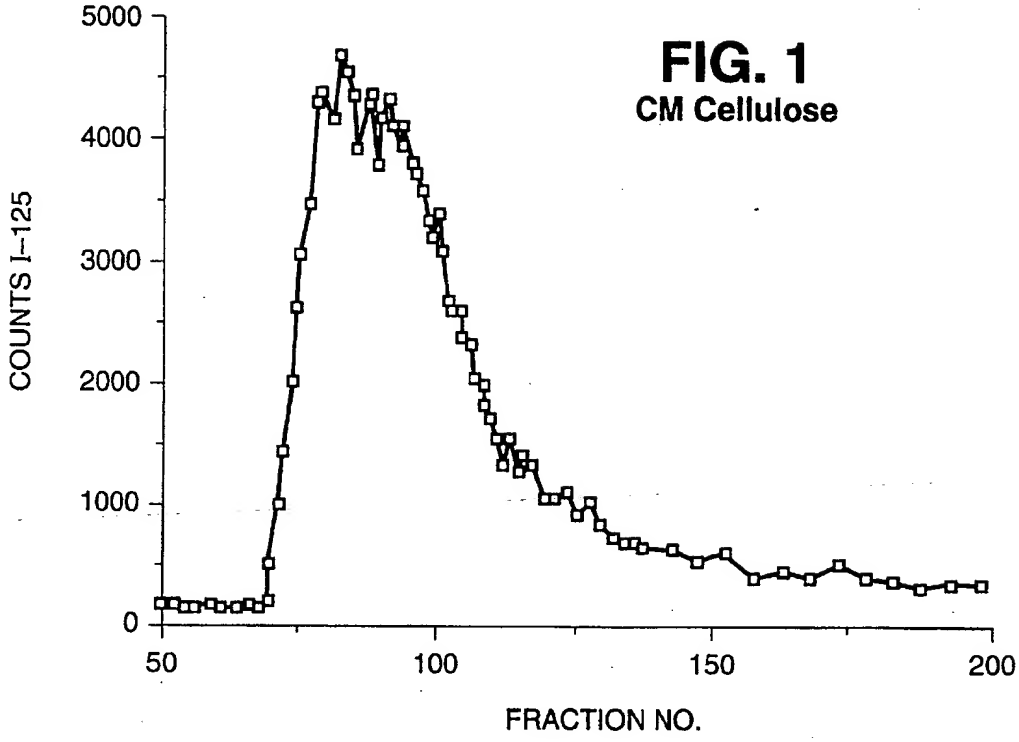


FIG. 1
CM Cellulose

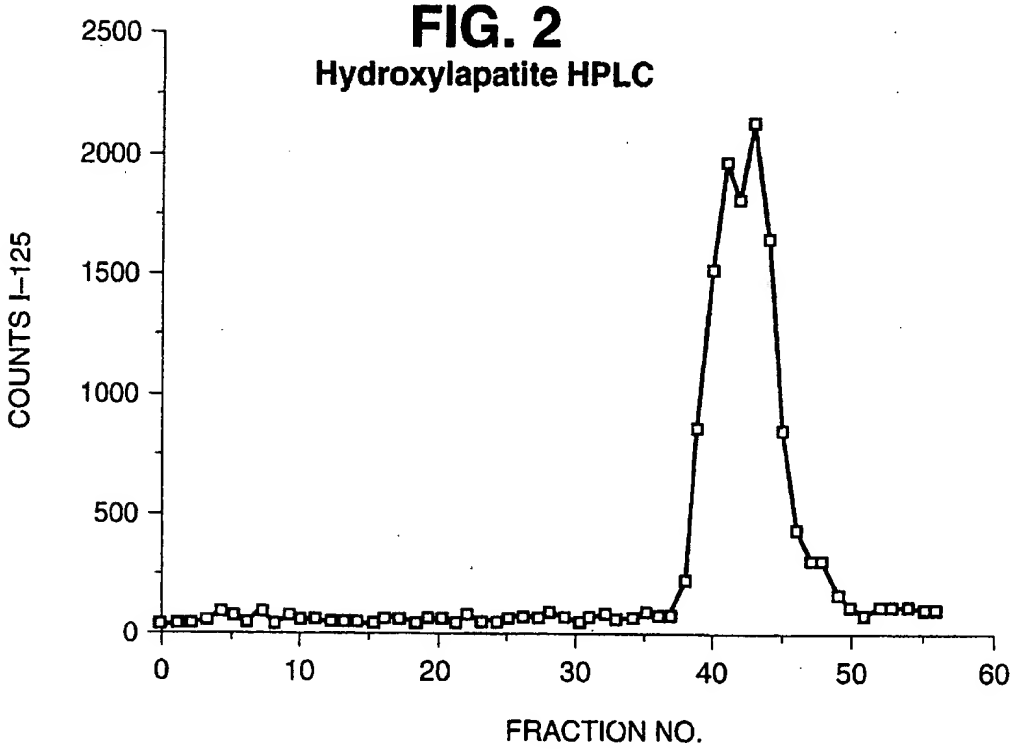


FIG. 2
Hydroxylapatite HPLC

FIG. 3

Mono S

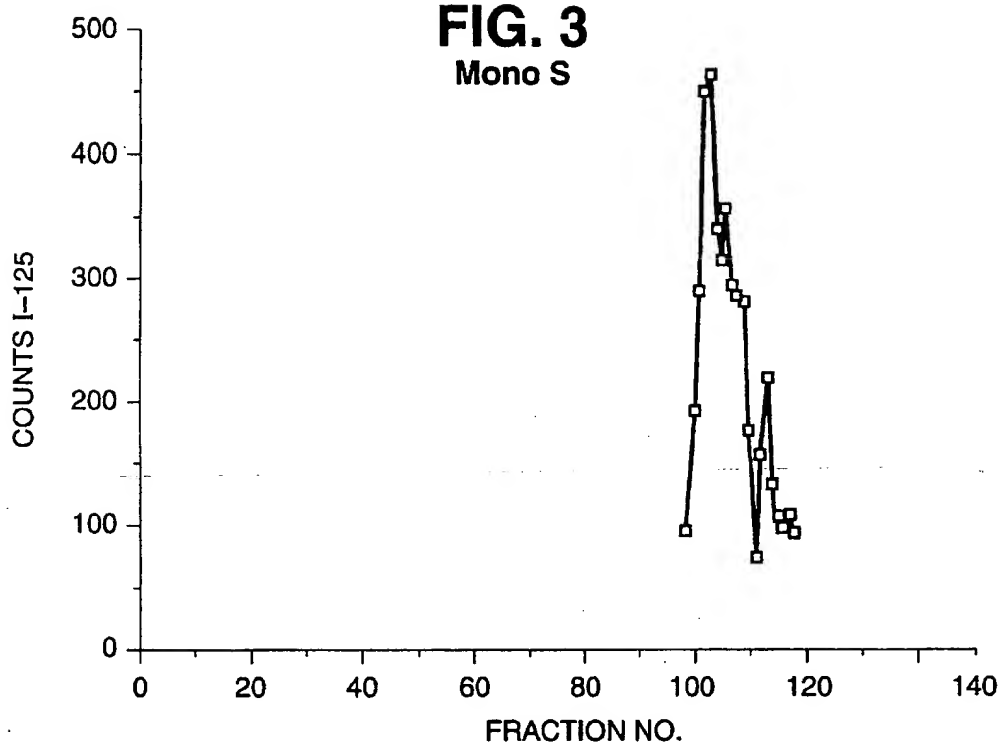
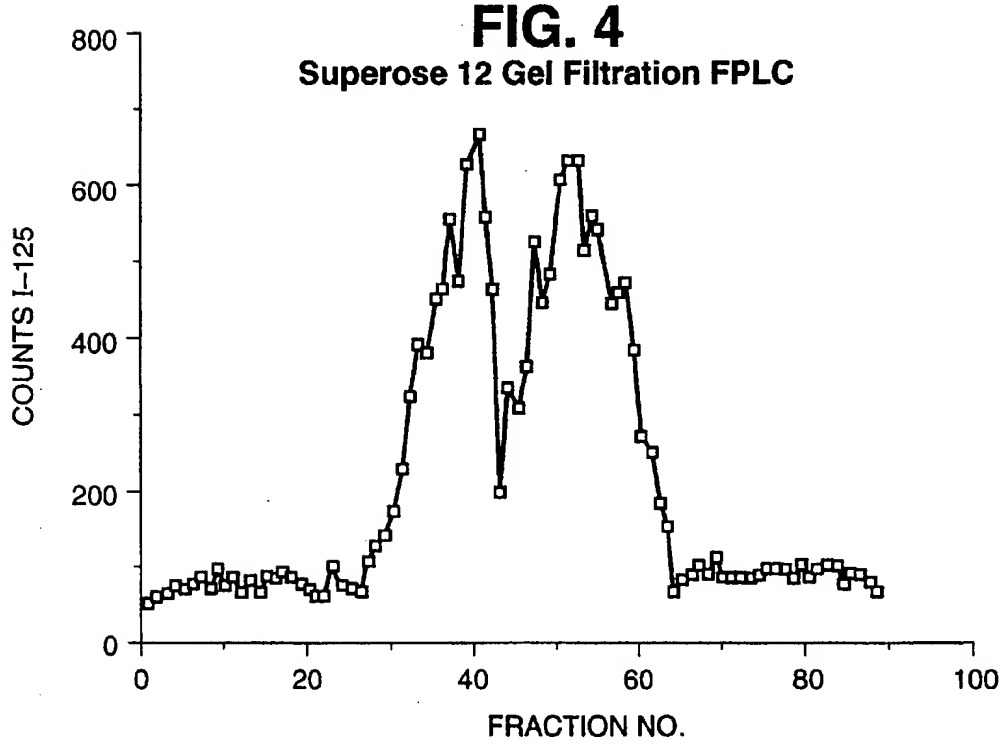


FIG. 4

Superose 12 Gel Filtration FPLC



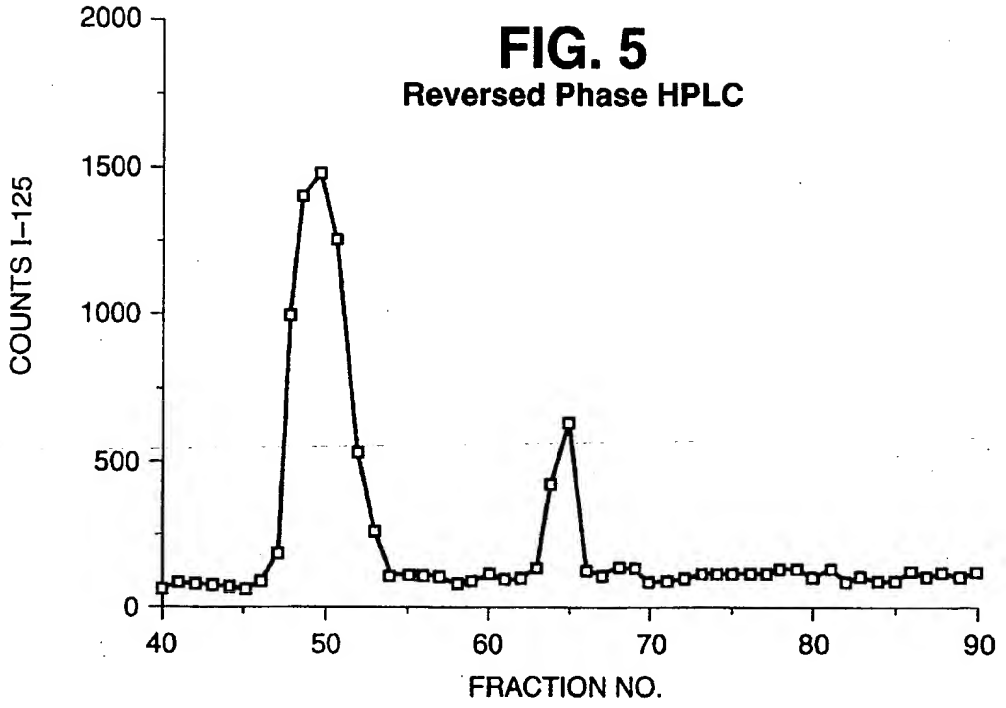


FIG. 5
Reversed Phase HPLC

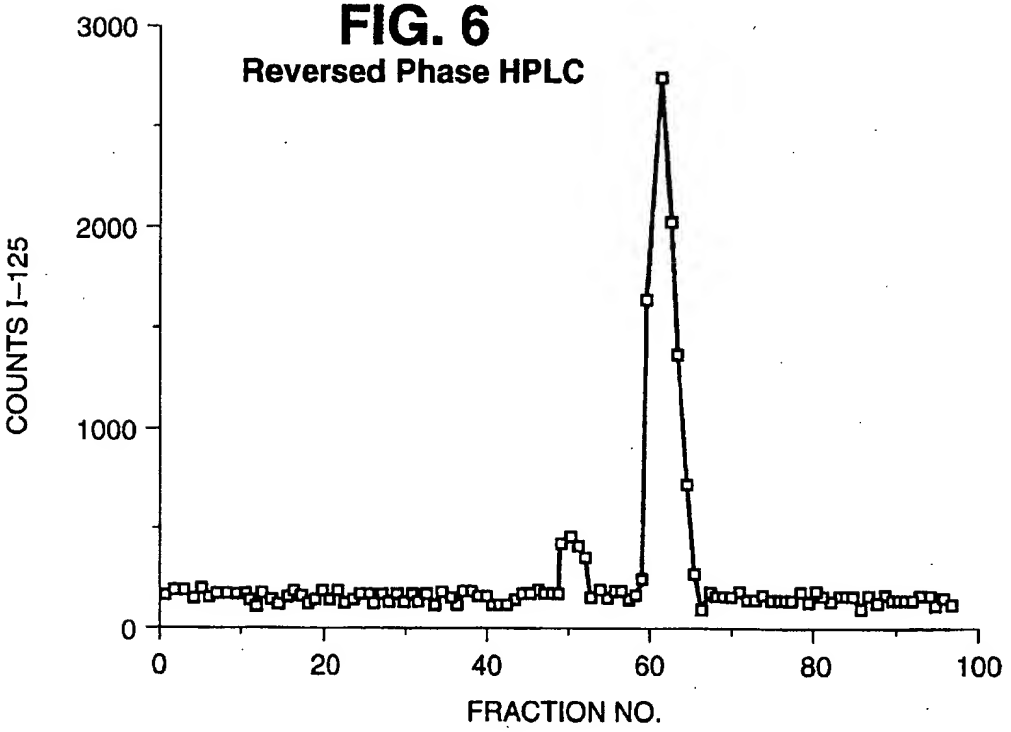


FIG. 6
Reversed Phase HPLC

FIG. 7

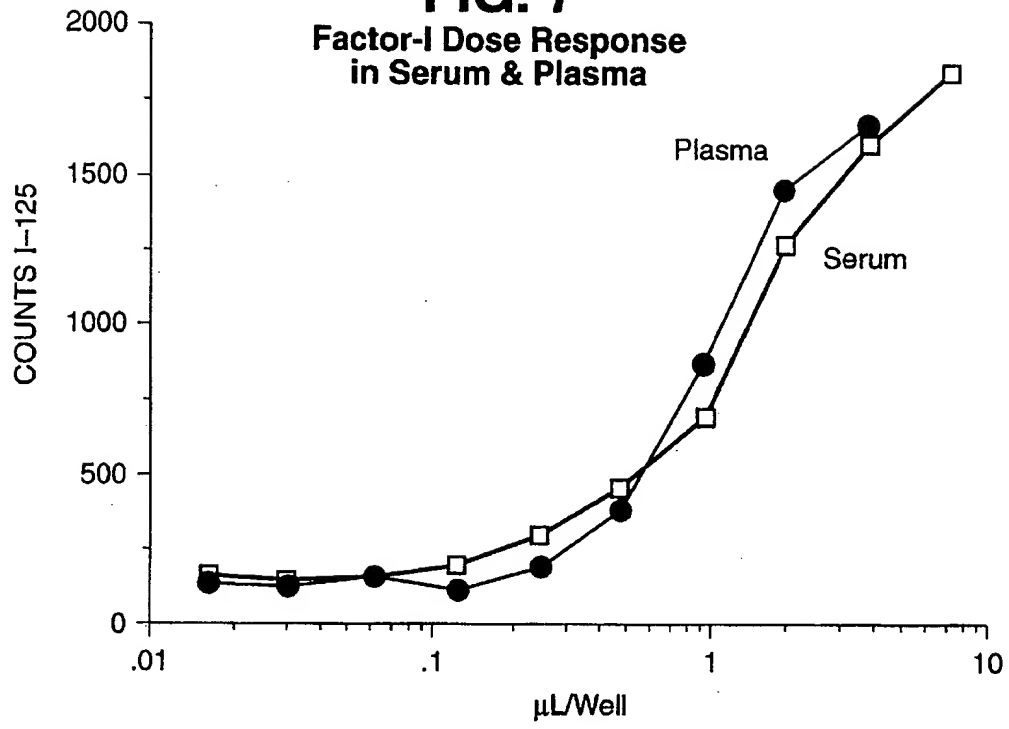

Factor-I Dose Response
in Serum & Plasma
Plasma
Serum
COUNTS I-125
2000
1500
1000
500
0
.01
.1
1
10
µL/Well

FIG. 8

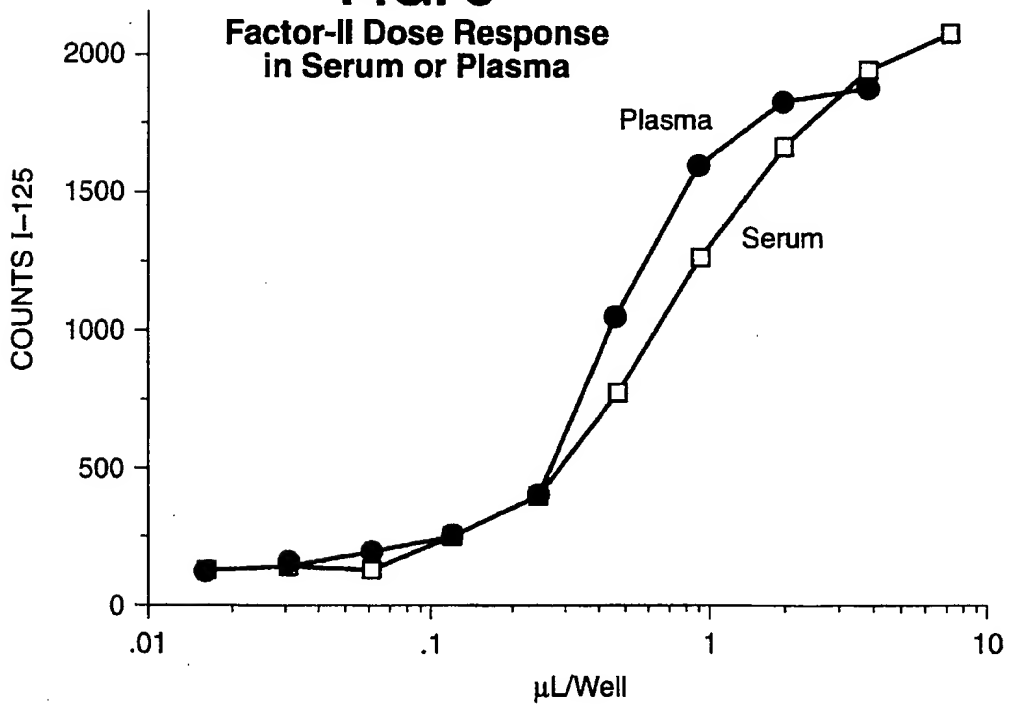

Factor-II Dose Response
in Serum or Plasma
Plasma
Serum
COUNTS I-125
2000
1500
1000
500
0
.01
.1
1
10
µL/Well

FIG. 9

	N-terminus		
GGF-I 01	F K G D A H T E	(SEQ ID NO: 1)	
	Trypsin peptides		
GGF-I 02	K/R A S L A D E Y E Y M X K *	(SEQ ID NO: 2)	
GGF-I 03	K/R T E T S S S G L X L K *	(SEQ ID NO: 3)	
GGF-I 04	K/R K L G E M W A E	(SEQ ID NO: 4)	HMG-1
GGF-I 05	K/R L G E K R A	(SEQ ID NO: 5)	HMG-1?
GGF-I 06	K/R I K S E H A G L S I G D T A K *	(SEQ ID NO: 6)	HMG-2
GGF-I 07	K/R A S L A D E Y E Y M R K *	(SEQ ID NO: 7)	
GGF-I 08	K/R I K G E H P G L S I G D V A K *	(SEQ ID NO: 8)	HMG-1
GGF-I 09	K/R M S E Y A F F V Q T X R *	(SEQ ID NO: 9)	HMG-2
GGF-I 10	K/R S E H P G L S I G D T A K *	(SEQ ID NO: 10)	HMG-1
GGF-I 11	K/R A G Y F A E X A R *	(SEQ ID NO: 11)	
GGF-I 12	K/R K L E F L X A K *	(SEQ ID NO: 12)	
GGF-I 13	K/R T T E M A S E Q G A	(SEQ ID NO: 13)	
GGF-I 14	K/R A K E A L A A L K *	(SEQ ID NO: 14)	
GGF-I 15	K/R F V L Q A K K *	(SEQ ID NO: 15)	
GGF-I 16	K/R L G E M W	(SEQ ID NO: 16)	HMG-1
	Protease V8 peptides		
GGF-I 17	E T Q P D P G Q I L K K V P M V I G A Y T	(SEQ ID NO: 169)	
GGF-I 18	E Y K C L K F K W F K K A T V M	(SEQ ID NO: 17)	
GGF-I 19	E A K Y F S K X D A	(SEQ ID NO: 18)	LH-alpha
GGF-I 20	E X K F Y V P	(SEQ ID NO: 19)	
GGF-I 21	E L S F A S V R L P G C P P G V D P M V S F P V A L	(SEQ ID NO: 20)	LH-beta

FIG. 10

A

GGF-I 01	F K G D A H T E	(SEQ ID NO: 1)
GGF-I 02	A S L A D E Y E Y M X K	(SEQ ID NO: 22)
GGF-I 03	T E T S S S G L X L K	(SEQ ID NO: 23)
GGF-I 07	A S L A D E Y E Y M R K	(SEQ ID NO: 24)
GGF-I 11	A G Y F A E X A R	(SEQ ID NO: 25)
GGF-I 13	T T E M A S E Q G A	(SEQ ID NO: 26)
GGF-I 14	A K E A L A A L K	(SEQ ID NO: 27)
GGF-I 15	F V L Q A K K	(SEQ ID NO: 28)
GGF-I 17	E T Q P D P G Q I L K K V P M V I G A Y T	(SEQ ID NO: 29)
GGF-I 18	E Y K C L K F K W F K K A T V M	(SEQ ID NO: 17)

B

GGF-I 20	E X K F Y V P	(SEQ ID NO: 19)
GGF-I 12	K L E F L X A K	(SEQ ID NO: 32)

FIG. 11

	Trypsin peptides		
GGF-II 01	K/R V H Q V W A A K *		(SEQ ID NO: 33)
GGF-II 02	K/R Y I F F M E P E A X S S G		(SEQ ID NO: 34)
GGF-II 03	K/R L G A W G P P A F P V X Y		(SEQ ID NO: 35)
GGF-II 04	K/R W F V V I E G K *		(SEQ ID NO: 36)
GGF-II 05	K/R A L A A A G Y D V E K *	Histone H1	(SEQ ID NO: 164)
GGF-II 06	K/R L V L R *		(SEQ ID NO: 165)
GGF-II 07	K/R X X Y P G Q I T S N	Trypsin	(SEQ ID NO: 166)
GGF-II 08	K/R A S P V S V G S V Q E L V Q R *		(SEQ ID NO: 37)
GGF-II 09	K/R V C L L T V A A P P T		(SEQ ID NO: 38)
GGF-II 10	K/R D L L L X V		(SEQ ID NO: 39)
	Lysyl Endopeptidase-C peptides		
GGF-II 11	K V H Q V W A A K *		(SEQ ID NO: 51)
GGF-II 12	K A S L A D S G E Y M X K*		(SEQ ID NO: 52)

FIG. 12

A

GGF-II 01	V H Q V W A A K	(SEQ ID NO: 45)
GGF-II 02	Y I F F M E P E A X S S G	(SEQ ID NO: 46)
GGF-II 03	L G A W G P P A F P V X Y	(SEQ ID NO: 47)
GGF-II 04	W F V V I E G K	(SEQ ID NO: 48)
GGF-II 08	A S P V S V G S V Q E L V Q R	(SEQ ID NO: 49)
GGF-II 09	V C L L T V A A P P T	(SEQ ID NO: 50)
GGF-II 11	K V H Q V W A A K	(SEQ ID NO: 51)
GGF-II 12	K A S L A D S G E Y M X K	(SEQ ID NO: 52)

B Novel Factor II Peptides - others

GGF-II 10	D L L L X V	(SEQ ID NO: 53)

FIG. 13

Comparison of BrdU-ELISA and [125 I]UdR Counting Method for the DNA Synthesis Assay in Schwann Cell Cultures

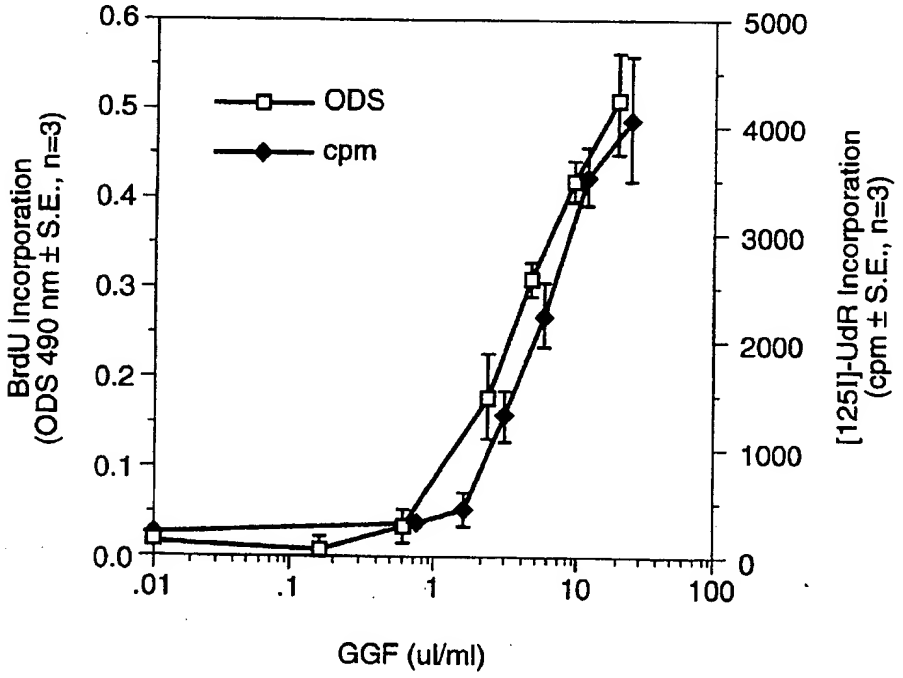


FIG. 14A

Comparison of Br-UdR Immunoreactivity and Br-UdR Labelled Cell Number

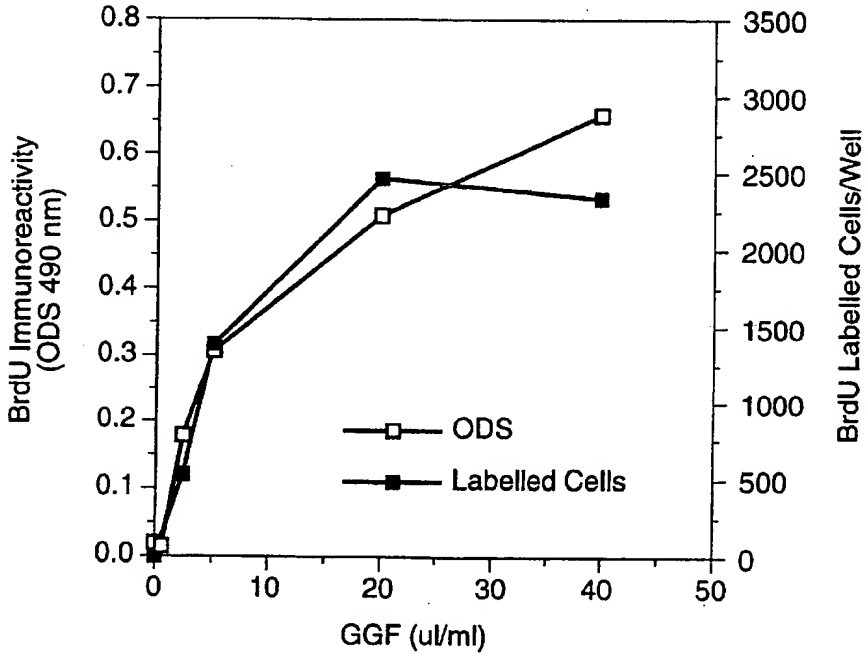


FIG. 14B

Comparison of Br-UdR Immunoreactivity and Br-UdR Labelled Cell Number

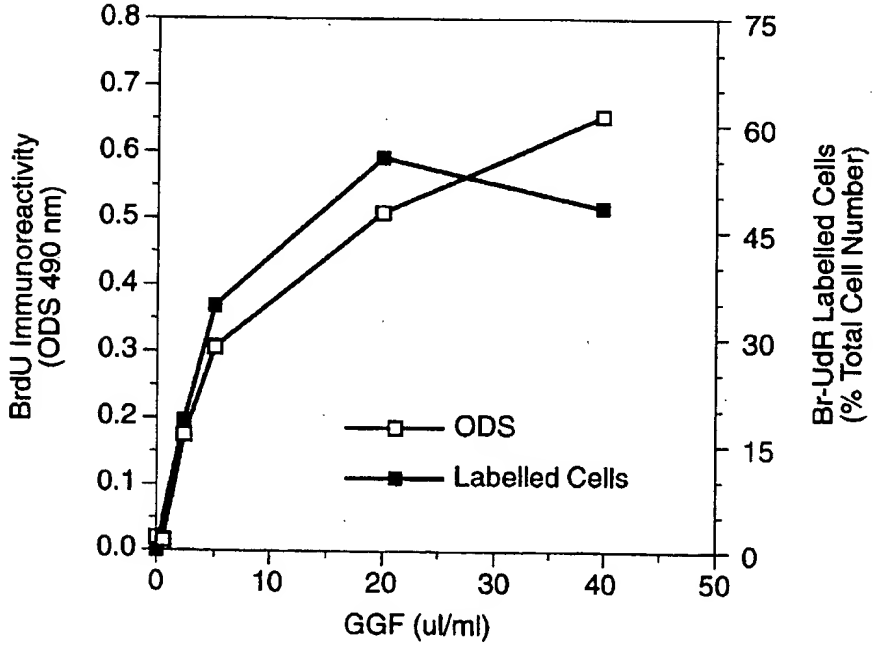


FIG. 15

Mitogenic Response of Rat Sciatic Nerve Schwann cell to GGFs

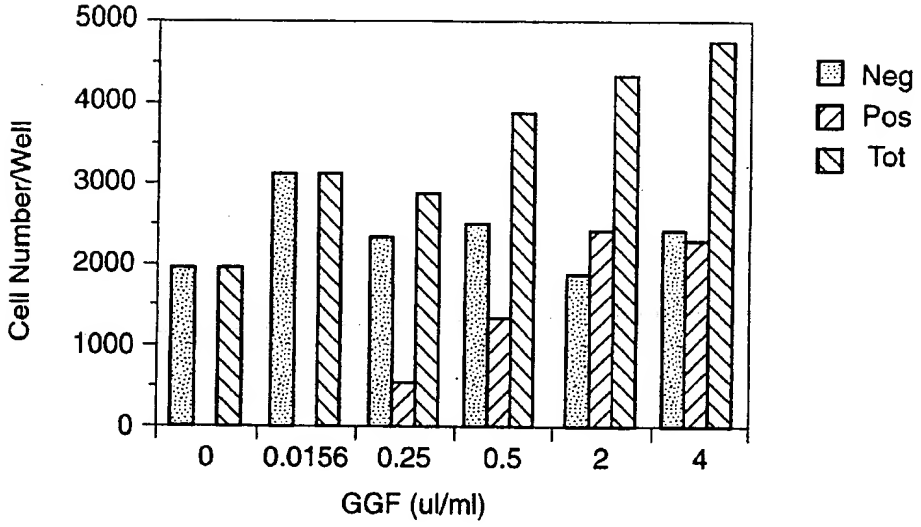


FIG. 16

DNA Synthesis in Rat Sciatic Nerve Schwann Cells and 3T3 Fibroblasts in the presence of GGFs

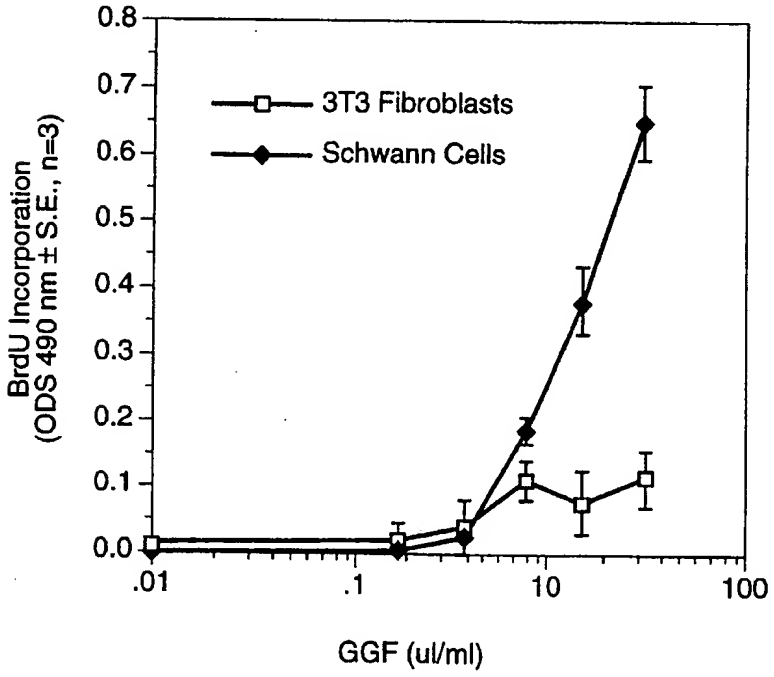


FIG. 17

Mitogenic Response of BHK 21 C13 Cells to FCS and GGFs

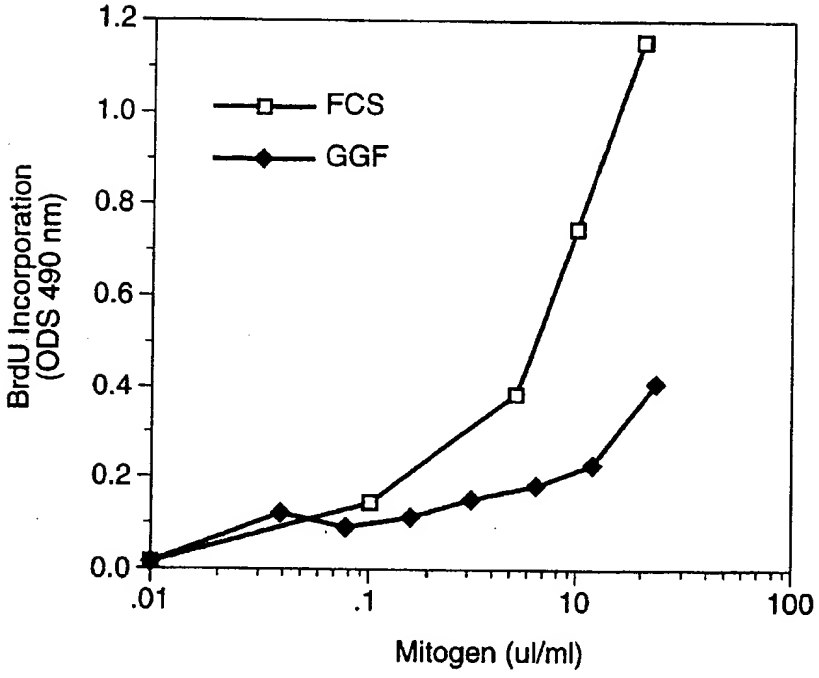


FIG. 18

Survival and Proliferation of BHK21 C13 Cell Microcultures After 48 Hours in Presence of GGFs

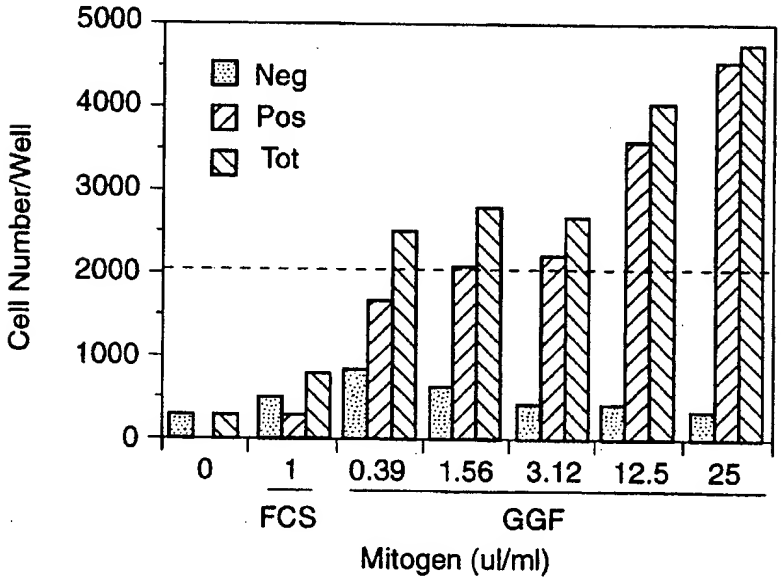


FIG. 19

Mitogenic Response of C6 Cells to FCS

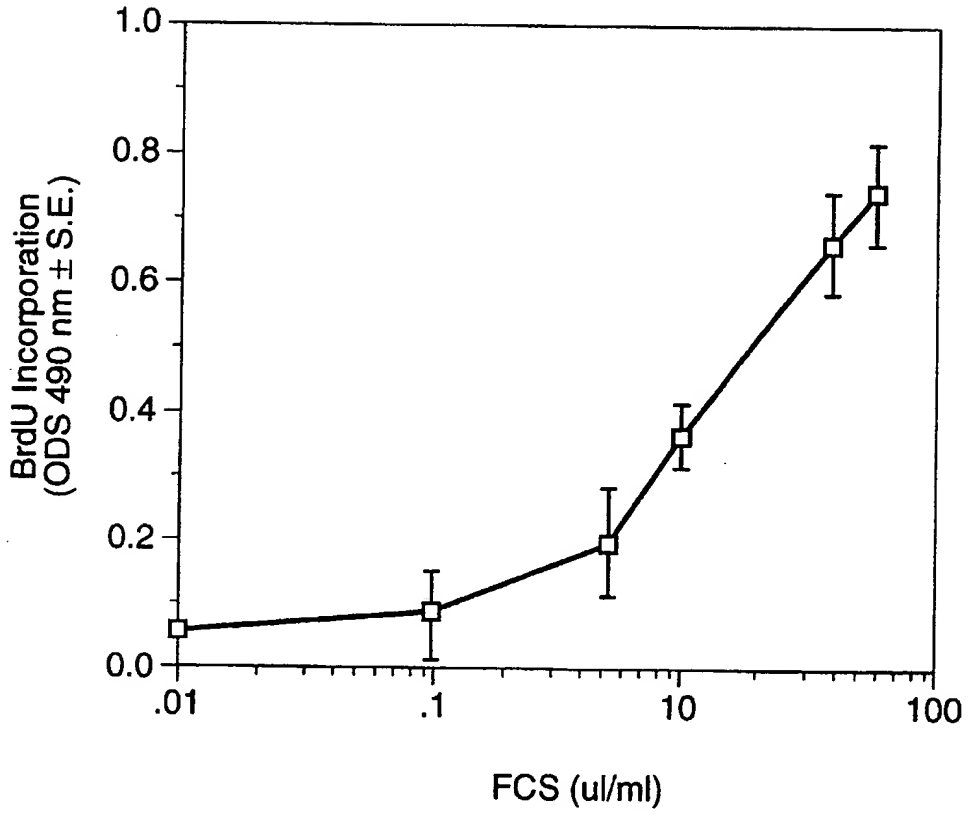


FIG. 20A

Mitogenic Response of C6 Cells to aFGF & GGFs

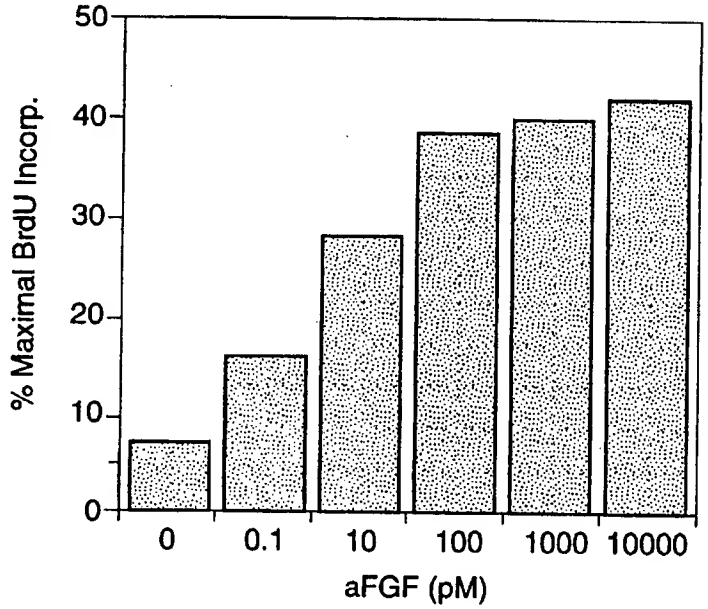


FIG. 20B

Mitogenic Response of C6 Cells to aFGF & GGFs

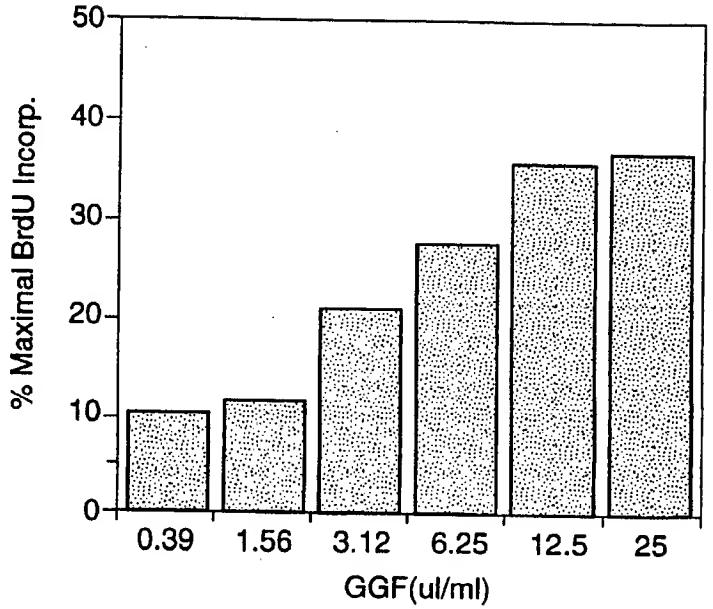


FIG. 21

Degenerate Oligonucleotide Probes for Factor I & Factor II

Oligo	Sequence	Peptide	
535	TTYAARGGNGAYGCNCAYAC!	GGFI-1	(SEQ ID NO: 54)
536	CATRTAYTCRTAYTCRTCNGC!	GGFI-2	(SEQ ID NO: 55)
537	TGYTCNGANGCCATYTCNGT!	GGFI-13	(SEQ ID NO: 56)
538	TGYTCRCTNGCCATYTCNGT!	GGFI-13	(SEQ ID NO: 57)
539	CCDATNACCATNGGNACYTT!	GGFI-17	(SEQ ID NO: 58)
540	GCNGCCCANACYTGRTGNAC!	GGFII-1	(SEQ ID NO: 59)
541	GCYTCNGGYTCCATRAARAA!	GGFII-2	(SEQ ID NO: 60)
542	CCYTCDATNACNACRAACCA!	GGFII-4	(SEQ ID NO: 61)
543	TCNGCRAARTANCCNGC!	GGFI-11	(SEQ ID NO: 62)
544	GCNGCNAGNGCYTCYTTNGC!	GGFI-14	(SEQ ID NO: 63)
545	GCNGCYAANGCYTCYTTNGC!	GGFI-14	(SEQ ID NO: 64)
546	TTYTTNGCYTGNAGNACRAA!	GGFI-15	(SEQ ID NO: 65)
551	TTYTTNGCYTGYAANACRAA!	GGFI-15	(SEQ ID NO: 66)
568	TGNACNAGYTCYTGNAC!	GGFII-8	(SEQ ID NO: 67)
569	TGNACYAAYTCYTGNAC!	GGFII-8	(SEQ ID NO: 68)
609	CATRTAYTCNCCNGARTCNGC!	GGFII-12	(SEQ ID NO: 69)
610	CATRTAYTCNCCRCTRTCNGC!	GGFII-12	(SEQ ID NO: 70)
649	NGARTCNGCYAANGANGCYTT!	GGFII-12	(SEQ ID NO: 71)
650	NGARTCNGCNAGNGANGCYTT!	GGFII-12	(SEQ ID NO: 72)
651	RCTRTCNGCYAANGANGCYTT!	GGFII-12	(SEQ ID NO: 73)
652	RCTRTCNGCNAGNGANGCYTT!	GGFII-12	(SEQ ID NO: 74)
653	NGARTCNGCYAARCTNGCYTT!	GGFII-12	(SEQ ID NO: 75)
654	NGARTCNGCNAGRCTNGCYTT!	GGFII-12	(SEQ ID NO: 76)
655	RCTRTCNGCYAARCTNGCYTT!	GGFII-12	(SEQ ID NO: 78)
656	RCTRCTNGCNAGRCTNGCYTT!	GGFII-12	(SEQ ID NO: 79)
659	ACNACNGARATGGCTCNNGA!	GGFI-13	(SEQ ID NO: 80)
660	ACNACNGARATGGCAGYNGA!	GGFI-13	(SEQ ID NO: 81)
661	CAYCARGTNTGGGCNGCNAA!	GGFII-1	(SEQ ID NO: 82)
662	TTYGTNGTNATHGARGGNAA!	GGFII-4	(SEQ ID NO: 83)
663	AARGGNGAYGCNCAYACNGA!	GGFI-1	(SEQ ID NO: 84)
664	GARGCNYTNGCNGCNYTNAA!	GGDI-14	(SEQ ID NO: 85)
665	GTNGGNTCNGTNCARGARYT!	GGFII-8	(SEQ ID NO: 86)
666	GTNGGNAGYGTNCARGARYT!	GGFII-8	(SEQ ID NO: 87)
694	NACYTTYTTNARHATYTGNCC!	GGFI-17	(SEQ ID NO: 88)

FIG. 22

Putative Bovine Factor II Gene Sequences

SEQ ID NO: 89:

```
TCTAA AAC TAC AGA GAC TGT ATT TTC ATG ATC ATC ATA GTT CTG TGA AAT ATA      53
      Asn Tyr Arg Asp Cys Ile Phe Met Ile Ile Ile Val Leu Xaa Asn Ile

CTT AAA CCG CTT TGG TCC TGA TCT TGT AGG AAG TCA GAA CTT CGC ATT          101
Leu Lys Pro Leu Trp Ser Xaa Ser Cys Arg Lys Ser Glu Leu Arg Ile

AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC          149
Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Ser Met Cys Lys Val Ile

AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG          197
Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Arg Ile Val Glu

TCA AAC GGT AAG AGA TGC CTA CTG CGT GCT ATT TCT CAG TCT CTA AGA          245
Ser Asn Gly Lys Arg Cys Leu Leu Arg Ala Ile Ser Gln Ser Leu Arg

GGA GTG ATC AAG GTA TGT GGT CAC ACT TGA ATC ACG CAG GTG TGT GAA          293
Gly Val Ile Lys Val Cys Gly His Thr Xaa Ile Thr Gln Val Cys Glu

ATC TCA TTG TGA ACA AAT AAA AAT CAT GAA AGG AAA ACT CTA TGT TTG          341
Ile Ser Cys Xaa Thr Asn Lys Asn His Glu Arg Lys Thr Leu Cys Leu

AAA TAT CTT ATG GGT CCT CCT GTA AAG CTC TTC ACT CCA TAA GGT GAA          389
Lys Tyr Leu Met Gly Pro Pro Val Lys Leu Phe Thr Pro Xaa Gly Glu

ATA GAC CTG AAA TAT ATA TAG ATT ATT T                                    417
Ile Asp Leu Lys Tyr Ile Xaa Ile Ile
```

FIG. 23A

PCR Primers for Factor I & Factor II

Degenerate PCR Primers

Oligo	Sequence	Peptide	
657	CCGAATTCTGCAGGARACNCARCCNGAYCCNGG!	GGFI-17	(SEQ ID NO: 90)
658	AAGGATCCTGCAGNGTRTANGCNCCHATNACCATNGG!	GGFI-17	(SEQ ID NO: 91)
667	CCGAATTCTGCAGGCNGAYTCNGGNGARTAYATG!	GGFII-12	(SEQ ID NO: 92)
668	CCGAATTCTGCAGGCNGAYATYGGNGARTAYAT!	GGFII-12	(SEQ ID NO: 93)
669	AAGGATCCTGCAGNNNCATRTAYTCNCCNGARTC!	GGFII-12	(SEQ ID NO: 94)
670	AAGGATCCTGCAGNNNCATRTAYTCNCCRRTRTC!	GGFII-12	(SEQ ID NO: 95)
671	CCGAATTCTGCAGCAYCARGTNTGGGCNGCNAA!	GGFII-1	(SEQ ID NO: 96)
672	CCGAATTCTGCAGATRTTYTTYATGGARCCNGARG!	GGFII-2	(SEQ ID NO: 97)
673	CCGAATTCTGCAGGGGGNCCNCCNGCNTTYCCNGT!	GGFII-3	(SEQ ID NO: 98)
674	CCGAATTCTGCAGTGGTTYGTNGTNATHGARGG!	GGFII-4	(SEQ ID NO: 99)
677	AAGGATCCTGCAGYTTNGCNGCCCANACYTGRTG!	GGFII-1	(SEQ ID NO: 100)
678	AAGGATCCTGCAGGCYTCNGGYTCCATRAARAA!	GGFII-2	(SEQ ID NO: 101)
679	AAGGATCCTGCAGACNGGRAANGCNGGNGGNCC!	GGFII-3	(SEQ ID NO: 102)
680	AAGGATCCTGCAGYTTNCCYTCDATNACNACRAAC!	GGFII-4	(SEQ ID NO: 103)
681	CATRTAYTCRTAYTCTCNGCAAGGATCCTGCAG!	GGFI-2	(SEQ ID NO: 104)
682	CCGAATTCTGCAGAARGGNGAYGCNCAYACNGA!	GGFI-1	(SEQ ID NO: 105)
683	GCNGCYAANGCYRCYTTNGCAAGGATCCTGCAG!	GGFI-14	(SEQ ID NO: 106)
684	GCNGCNAGNGCYTCYTTNGCAAGGATCCTGCAG!	GGFI-14	(SEQ ID NO: 107)
685	TCNGCRAARTANCCNGCAAGGATCCTGCAG!	GGFII-1	(SEQ ID NO: 108)

FIG. 23B

PCR Primers for Factor I & Factor II

Unique PCR Primers for Factor II

Oligo	Sequence	Comment	
711	CATCGATCTGCAGGCTGATTCTGGAGAATATATGTGCA!	3' RACE	(SEQ ID NO: 109)
712	AAGGATCCTGCAGCCACATCTCGAGTCGACATCGATT!	3' RACE	(SEQ ID NO: 110)
713	CCGAATTCTGCAGTGATCAGCAAACTAGGAAATGACA!	3' RACE	(SEQ ID NO: 111)
721	CATCGATCTGCAGCCTAGTTTGCTGATCACTTTGCAC!	5' RACE	(SEQ ID NO: 112)
722	AAGGATCCTGCAGTATATTCTCCAGAATCAGCCAGTG!	5' RACE;ANCHORED	(SEQ ID NO: 113)
725	AAGGATCCTGCAGGCACGCAGTAGGCATCTCTTA!	EXON A	(SEQ ID NO: 114)
726	CCGAATTCTGCAGCAGAACTTCGCATTAGCAAAGC!	EXON A	(SEQ ID NO: 115)
771	CATCCCGGGATGAAGAGTCAGGAGTCTGTGGCA!	EXONS B+A	(SEQ ID NO: 116)
772	ATACCCGGGCTGCAGACAATGAGATTTCACACACCTGCG!		(SEQ ID NO: 117)
773	AAGGATCCTGCAGTTTGGAACCTGCCACAGACTCCT!	ANCHORED	(SEQ ID NO: 118)
776	ATACCCGGGCTGCAGATGAGATTTCACACACCTGCGTGA!	EXONS B+A	(SEQ ID NO: 119)

FIG. 24

Summary of Contiguous GGF-II cDNA Structures & Sequences

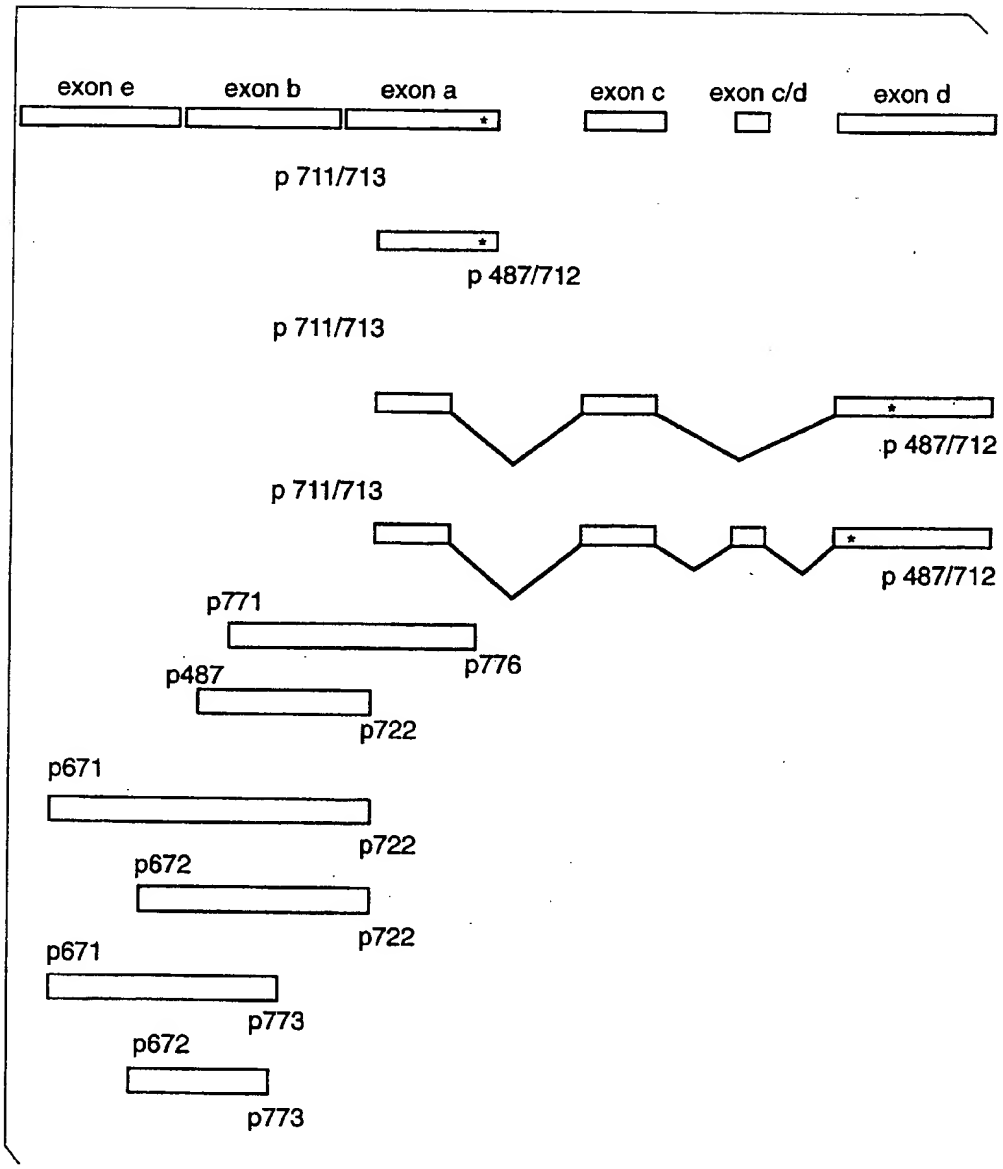


FIG. 25

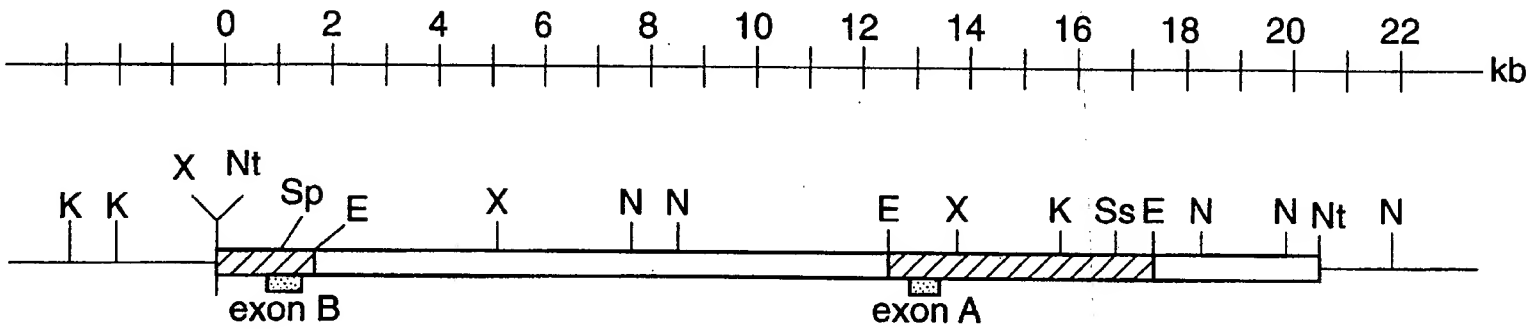

0
2
4
6
8
10
12
14
16
18
20
22
kb
K
K
X
Nt
Sp
E
X
N
N
E
X
K
Ss
E
N
N
Nt
N
exon B
exon A

FIG. 26

Alternative Gene Products of Putative Bovine GGF-II

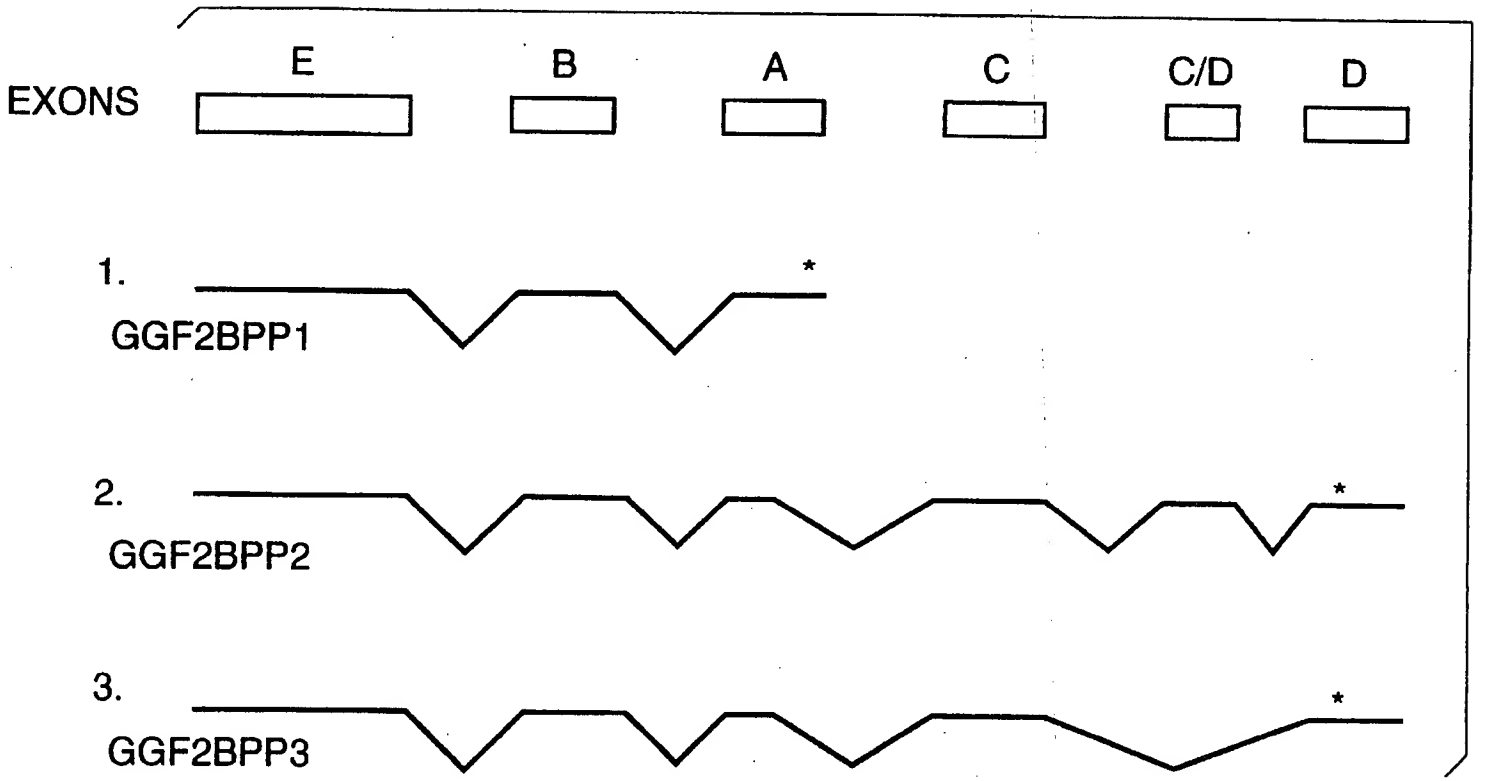


FIG. 27

GGF-II Peptides Identified in Deduced Amino Acid Sequences of Putative Bovine GGF-II Proteins

Peptide	Pos.		Sequence match	ID Sequences
II-1			VHQVWAAK	
	1:		HQVWAAK AAGLK	(SEQ ID NO:120)
II-10			DLLLXV	
	14:	GGLKK	dslltv RLGAW	(SEQ ID NO:121)
II-03			LGAWGPPAFPVXY	(SEQ ID NO:122)
	21:	LLTVR	lgawghpafpscg RLKED	(SEQ ID NO:123)
II-02			YIFFMEPEAXSSG	(SEQ ID NO:124)
	41:	KEDSR	YIFFMEPEANSSG GPGRL	(SEQ ID NO:125)
II-6			LVLR	
	103:	VAGSK	LVLR CETSS	(SEQ ID NO:126)
I-18			EYKCLKFKWFKKATVM	(SEQ ID NO:127)
	112:	CETSS	eysslkfkwfkngsel SRKNK	(SEQ ID NO:128)
II-12			KASLADSGEYMXK	(SEQ ID NO:129)
	151:	ELRIS	KASLADSGEYMCK VISKL	(SEQ ID NO:130)
I-07			ASLADEYEYMRK	(SEQ ID NO:131)
	152:	LRISK	asladsgeymck VISKL	(SEQ ID NO:132)

FIG. 28A

SEQ ID NO: 133:

```
CCTGCAG CAT CAA GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG  55
       His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu

CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC TGC        103
Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys

GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAG        151
Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu

GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT CCC CCC        199
Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro

TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT GTG        247
Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala Val

CAA CGG TGC GCC TTG CCT CCC CGC TTG AAA GAG ATG AAG AGT CAG GAG        295
Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu

TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA        343
Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu

TAC TCC TCT CTC AAG TTC AAG TGG TTC AAG AAT GGG AGT GAA TTA AGC        391
Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser

CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG GGG AAG        439
Arg Lys Asn Lys Pro Glu Asn Ile Lys Ile Gln Lys Arg Pro Gly Lys

TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT        487
Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr

ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC        535
Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn

ATC ACC ATT GTG GAG TCA AAC GGT AAG AGA TGC CTA CTG CGT GCT ATT        583
Ile Thr Ile Val Glu Ser Asn Gly Lys Arg Cys Leu Leu Arg Ala Ile

TCT CAG TCT CTA AGA GGA GTG ATC AAG GTA TGT GGT CAC ACT                625
Ser Gln Ser Leu Arg Gly Val Ile Lys Val Cys Gly His Thr

TGAATCACGC AGGTGTGTGA AATCTCATTG TGAACAAATA AAAATCATGA AAGGAAAAAA      685

AAAAAAAAAA AATCGATGTC GACTCGAGAT GTGGCTGCAG GTCGACTCTA GAGGATCCC       744
```

FIG. 28B

Nucleotide Sequences & Deduced Amino Acid Sequences of GGF2BPP2

SEQ ID NO: 134:

```
CCTGCAG CAT CAA GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG   55
       His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu

CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC TGC         103
Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys

GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAG         151
Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu

GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT CCC CCC         199
Ala Lys Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro

TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT GTG         247
Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala Val

CAA CGG TGC GCC TTG CCT CCC CGC TTG AAA GAG ATG AAG AGT CAG GAG         295
Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu

TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA         343
Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu

TAC TCC TCT CTC AAG TTC AAG TGG TTC AAG AAT GGG AGT GAA TTA AGC         391
Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser

CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG GGG AAG         439
Arg Lys Asn Lys Gly Gly Asn Ile Lys Ile Gln Lys Arg Pro Gly Lys

TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT         487
Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr

ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC         535
Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn
```

FIG. 28C

Nucleotide Sequences & Deduced Amino Acid Sequences of GG2BPP2

```
ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG ACA          583
Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly Thr

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT          631
Ser His Leu Val Lys Ser Ala Glu Lys Glu Lys Thr Phe Cys Val Asn

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC          679
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr


TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT          727
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn

GTG CCC ATG AAA GTC CAA ACC CAA GAA AGT GCC CAA ATG AGT TTA CTG          775
Val Pro Met Lys Val Gln Thr Gln Glu Ser Ala Gln Met Ser Leu Leu

GTG ATC GCT GCC AAA ACT ACG TAATGGCCAG CTTCTACAGT ACGTCCACTC             826
Val Ile Ala Ala Lys Thr Thr

CCTTTCTGTC TCTGCCTGAA TAGCGCATCT CAGTCGGTGC CGCTTTCTTG TTGCCGCATC       886

TCCCCTCAGA TTCCTCCTAG AGCTAGATGC GTTTTACCAG GTCTAACATT GACTGCCTCT       946

GCCTGTCGCA TGAGAACATT AACACAAGCG ATTGTATGAC TTCCTCTGTC CGTGACTAGT      1006

GGGCTCTGAG CTACTCGTAG GTGCGTAAGG CTCCAGTGTT TCTGAAATTG ATCTTGAATT      1066

ACTGTGATAC GACATGATAG TCCCTCTCAC CCAGTGCAAT GACAATAAAG GCCTTGAAAA      1126

GTCAAAAAAA AAAAAAAAAA AAAAAATCGA TGTCGACTCG AGATGTGGCT GCAGGTCGAC      1186

TCTAGAG                                                                1193
```

FIG. 28D

Nucleotide Sequences & Deduced Amino Acid Sequences of GGF2BPP3

SEQ ID NO: 135:

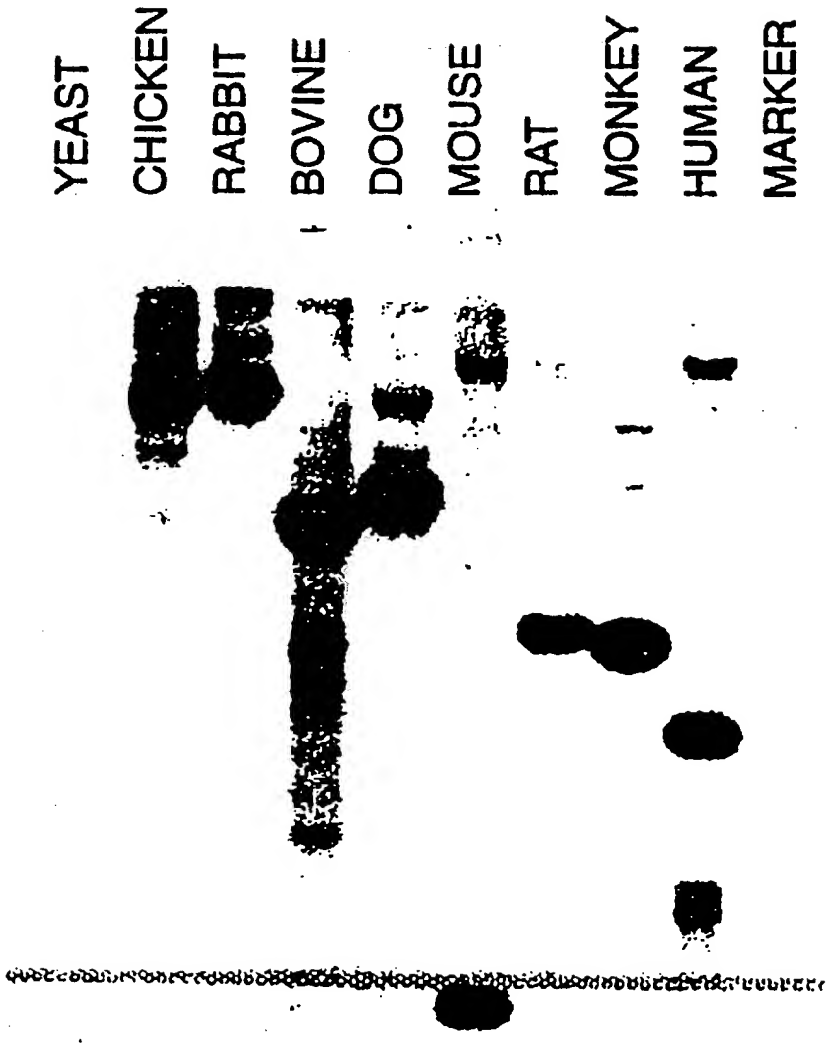
```
CCTGCAG CAT CAA GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG  55
       His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu

CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC TGC        103
Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys

GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAG        151
Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu

GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT CCC CCC        199
Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro

TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT GTG        247
Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala Val

CAA CGG TGC GCC TTG CCT CCC CGC TTG AAA GAG ATG AAG AGT CAG GAG        295
Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu

TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA        343
Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu

TAC TCC TCT CTC AAG TTC AAG TGG TTC AAG AAT GGG AGT GAA TTA AGC        391
Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser

CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG GGG AAG        439
Arg Lys Asn Lys Pro Glu Asn Ile Lys Ile Gln Lys Arg Pro Pro Lys

TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT        487
Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr
```

FIG. 28E

Nucleotide Sequences & Deduced Amino Acid Sequences of GGF2BPP3

```
ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC          535
Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn

ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG ACA          583
Ile Arg Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly Thr

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT          631
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC          679
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr

TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC          727
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr

GTA ATG GCC AGC TTC TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT          775
Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro

GAA TAGCGCATCT CAGTCGGTGC CGCTTTCTTG TTGCCGCATC TCCCCTCAGA TTCCGCCTAG   838
Glu

AGCTAGATGC GTTTTACCAG GTCTAACATT GACTGCCTCT GCCTGTCGCA TGAGAACATT      898

AACACAAGCG ATTGTATGAC TTCCTCTGTC CGTGACTAGT GGGCTCTGAG CTACTCGTAG      958

GTGCGTAAGG CTCCAGTGTT TCTGAAATTG ATCTTGAATT ACTGTGATAC GACATGATAG     1018

TCCCTCTCAC CCAGTGCAAT GACAATAAAG GCCTTGAAAA GTCAAAAAAA AAAAAAAAAA     1078

AAAAATCGAT GTCGACTCGA GATGTGGCTG                                      1108
```

FIG. 29


YEAST
CHICKEN
RABBIT
BOVINE
DOG
MOUSE
RAT
MONKEY
HUMAN
MARKER

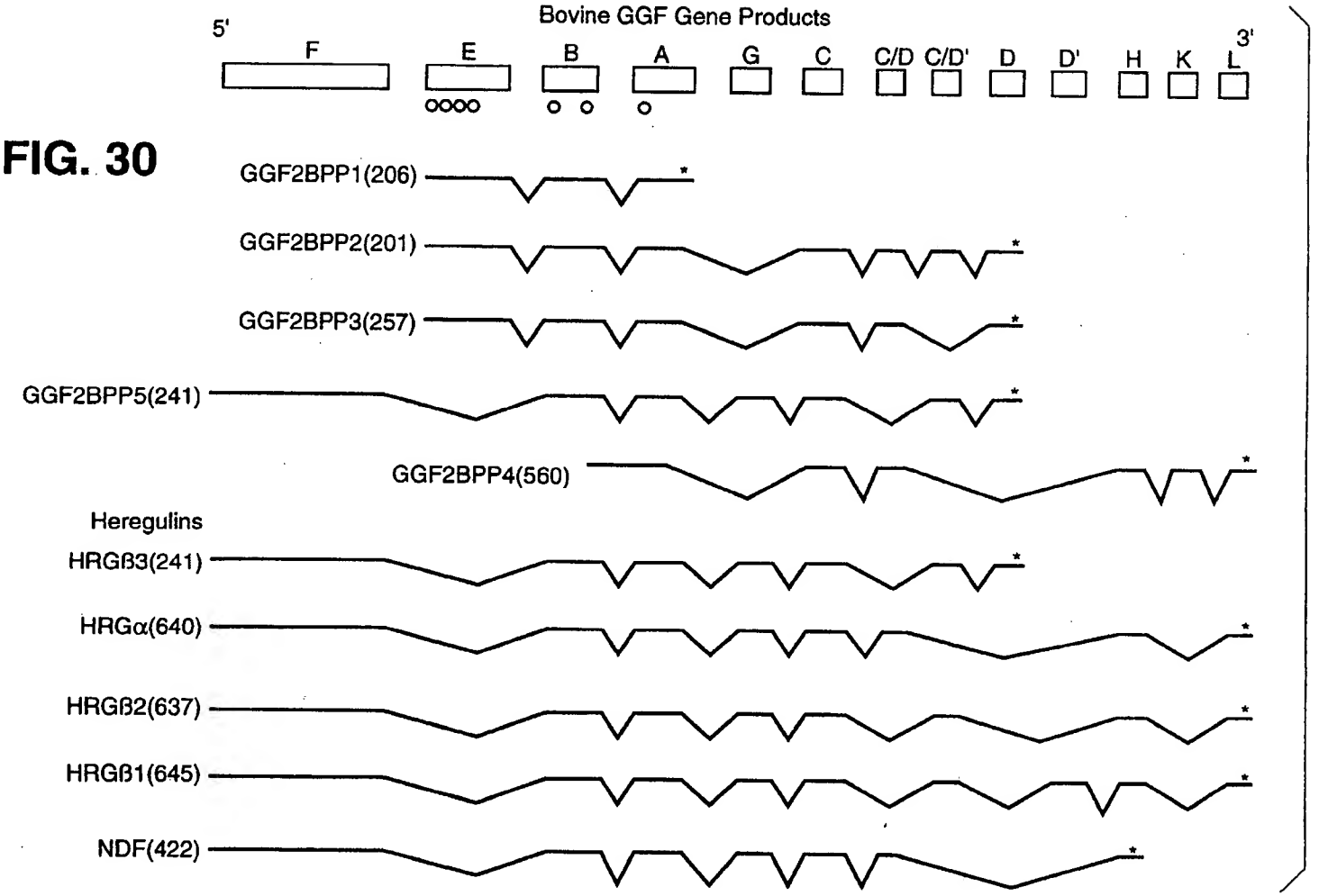

Bovine GGF Gene Products
5'
3'
F
E
B
A
G
C
C/D
C/D'
D
D'
H
K
L
GGF2BPP1(206)
GGF2BPP2(201)
GGF2BPP3(257)
GGF2BPP5(241)
GGF2BPP4(560)
Heregulins
HRGß3(241)
HRGα(640)
HRGß2(637)
HRGß1(645)
NDF(422)

FIG. 30

FIG. 31A

Coding Segments of Glial Growth Factor/Heregulin Gene

CODING SEGMENT F: (SEQ ID NO: 136 (bovine) and 173 (human))

```
AGTTTCCCCC CCCAACTTGT CGGAACTCTG GGCTCGCGCG CAGGGCAGGA GCGGAGCGGC      60

GGCGGCTGCC CAGGCGATGC GAGCGCGGGC CGGACGGTAA TCGCCTCTCC CTCCTCGGGC     120

TGCGAGCGCG CCGGACCGAG GCAGCGACAG GAGCGGACCG CGGCGGGAAC CGAGGACTCC     180

CCAGCGGCGC GCCAGCAGGA GCCACCCCGC GAGNCGTGCG ACCGGGACGG AGCGCCCGCC     240

AGTCCCAGGT GGCCCGGACC GCACGTTGCG TCCCCGCGCT CCCCGCCGGC GACAGGAGAC     300

GCTCCCCCCC ACGCCGCGCG CGCCTCGGCC CGGTCGCTGG CCCGCCTCCA CTCCGGGGAC     360
                |||| | |||||| ||  ||| |||| | | | |  ||| |||||
                CGCGAG CGCCTCAGCG CGGCCGCTCG CTCTC..CCC CTCGAGGGAC

AAACTTTTCC CGAAGCCGAT CCCAGCCCTC GGACCCAAAC TTGTCGCGCG TCGCCTTCGC     420
|||||||||| | || ||||| || ||||||  ||||| ||              |||||| |||
AAACTTTTCC CAAACCCGAT CCGAGCCCTT GGACCAAA.. .........C TCGCCTGCGC

                                                  Met Ser Glu Arg Arg
CGGGAGCCGT CCGCGCAGAG CGTGCACTTC TCGGGCGAG ATG TCG GAG CGC AGA       474
|| |||||||  |||||  ||||  ||  | | ||  || ||||||  |||  ||  |||  |||  | |
CGAGAGCCGT CCGCGTAGAG CGCTC.CGTC TCCGGCGAG ATG TCC GAG CGC AAA
                                                              K

Glu Gly Lys Gly Lys Gly Lys Gly Gly Lys Lys Asp Arg Gly Ser Gly
GAA GGC AAA GGC AAG GGG AAG GGC GGC AAG AAG GAC CGA GGC TCC GGG       522
|||  |||  | |  |||  ||  |||  |||  |||      |||  |||  ||  |||  |||  |||  ||
GAA GGC AGA GGC AAA GGG AAG GGC AAG AAG AAG GAG CGA GGC TCC GGC
       R                       K           E

Lys Lys Pro Val Pro Ala Ala Gly Gly Pro Ser Pro Ala
AAG AAG CCC GTG CCC GCG GCT GGC GGC CCG AGC CCA G                    559
|||  |||  ||  |  |  ||  |||  ||  |||  ||  |  |  |||. |||  |
AAG AAG CCG GAG TCC GCG GCG GGC AGC CAG AGC CCA G
          E   S
```

FIG. 31B

CODING SEGMENT E:(SEQ ID NO: 137)

```
 CC CAT CAN GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG        47
    His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser

CTG CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC        95
Leu Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser

TGC GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC       143
Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro

GAG GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT CCC       191
Glu Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro

CCC TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT       239
Pro Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala

GTG CAA CGG TGC G                                                    252
Val Gln Arg Cys
```

FIG. 31C

CODING SEGMENT B: (SEQ ID NO: 138 (bovine) and 174 (human))

```
Leu Pro Pro Arg Leu Lys Glu His Lys Ser Gln Glu Ser Val Ala Gly
CCT TGC CTC CCC GCT TGA AAG AGA TGA AGA GTC AGG AGT CTG TGG CAG      48
||| ||| ||| ||| | | ||| ||| ||| ||| | | | ||| | | | |  | |||
CCT TGC CTC CCC GAT TGA AAG AGA TGA AAA GCC AGG AAT CGG CTG CAG
            Q                                       A

Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu
GTT CCA AAC TAG TGC TTC GGT GCG AGA CCA GTT CTG AAT ACT CCT CTC      96
||| ||| ||| ||| | | ||| ||| | | | | ||| ||| ||| ||| ||| ||| |||
GTT CCA AAC TAG TCC TTC GGT GTG AAA CCA GTT CTG AAT ACT CCT CTC

Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser Arg Lys Asn Lys
TCA AGT TCA AGT GGT TCA AGA ATG GGA GTG AAT TAA GCC GAA AGA ACA     144
|||  | ||| ||| ||| ||| ||| ||| ||| || ||| | |  | ||| | | |||
TCA GAT TCA AGT GGT TCA AGA ATG GGA ATG AAT TGA ATC GAA AAA ACA
R                           N       N

Pro Gly Asn Ile Lys Ile Gln Lys Arg Pro Gly
AAC CAC AAA ACA TCA AGA TAC AGA AAA GGC CGG G                      178
||| ||| ||| | | ||| ||| ||| | | ||| || | | |
AAC CAC AAA ATA TCA AGA TAC AAA AAA AGC CAG G
                          K
```

FIG. 31D

CODING SEGMENT A: (SEQ ID NO: 139 (bovine) and 175 (human))

```
   Lys Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly
 G AAG TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA        46
   ||| ||| ||| ||| ||| ||| | | ||| ||  ||| ||| ||| ||| ||| |||
 G AAG TCA GAA CTT CGC ATT AAC AAA GCA TCA CTG GCT GAT TCT GGA
                           N

Glu Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser
GAA TAT ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT      94
||  ||| ||| ||| ||| ||| ||| ||| |||  || ||| ||| ||| ||| ||| |||
GAG TAT ATG TGC AAA GTG ATC AGC AAA TTA GGA AAT GAC AGT GCC TCT

Ala Asn Ile Thr Ile Val Glu Ser Asn Ala
GCC AAC ATC ACC ATT GTG GAG TCA AAC G                              122
||| ||  ||| ||| ||  ||| ||  ||| ||| |
GCC AAT ATC ACC ATC GTG GAA TCA AAC G
```

FIG. 31E

CODING SEGMENT A': (SEQ ID NO: 140)

```
TCTAAAACTA CAGAGACTGT ATTTTCATGA TCATCATAGT TCTGTGAAAT ATACTTAAAC      60

CGCTTTGGTC CTGATCTTGT AGG AAG TCA GAA CTT CGC ATT AGC AAA GCG         110
                          Lys Ser Glu Leu Arg Ile Ser Lys Ala

TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC AGC AAA CTA       158
Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys Leu

GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG TCA AAC GGT       206
Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn Gly

AAG AGA TGC CTA CTG CGT GCT ATT TCT CAG TCT CTA AGA GGA GTG ATC       254
Lys Arg Cys Leu Leu Arg Ala Ile Ser Gln Ser Leu Arg Gly Val Ile

AAG GTA TGT GGT CAC ACT TGAATCACGC AGGTGTGTGA AATCTCATTG              302
Lys Val Cys Gly His Thr

TGAACAAATA AAAATCATGA AAGGAAAACT CTATGTTTGA AATATCTTAT GGGTCCTCCT     362

GTAAAGCTCT TCACTCCATA AGGTGAAATA GACCTGAAAT ATATATAGAT TATTT          417
```

FIG. 31F

CODING SEGMENT G: (SEQ ID NO: 141 (bovine) and 176 (human))

```
Glu Ile Thr Thr Gly Met Pro Ala Ser Thr Glu Thr Ala Tyr Val Ser
 AG ATC ACC ACT GGC ATG CCA GCC TCA ACT GAG ACA GCG TAT GTG TCT        47
 || ||| | | ||| ||  ||| ||| ||| ||| ||| ||    | ||  ||| ||| |||
 AG ATC ATC ACT GGT ATG CCA GCC TCA ACT GAA GGA GCA TAT GTG TCT
        I                                   G

Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Thr Asn Thr
TCA GAG TCT CCC ATT AGA ATA TCA GTA TCA ACA GAA GGA ACA AAT ACT      95
||| ||| ||| ||| ||| ||| ||| ||| ||| ||  ||| ||| |||  || ||| |||
TCA GAG TCT CCC ATT AGA ATA TCA GTA TCC ACA GAA GGA GCA AAT ACT
                                                    A

Ser Ser Ser
TCT TCA T                                                          102
||| ||| |
TCT TCA T
```

FIG. 31G

CODING SEGMENT C: (SEQ ID NO: 160 (bovine) and 177 (human))

```
    Thr Ser Thr Ser Thr Ala Gly Thr Ser His Leu Val Lys Cys Ala
CC  ACA TCC ACA TCT ACA GCT GGG ACA AGC CAT CTT GTC AAG TGT GCA      47
|   ||| ||  ||| ||  ||   ||  ||| ||| ||| ||| ||| ||  ||  ||| ||
CT  ACA TCT ACA TCC ACC ACT GGG ACA AGC CAT CTT GTA AAA TGT GCG
                        T

Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys Phe Met Val
GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGC GAG TGC TTC ATG GTG      95
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||  ||| ||| ||| ||| |||
GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGG GAG TGC TTC ATG GTG

Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys
AAA GAC CTT TCA AAT CCC TCA AGA TAC TTG TGC                        128
||| ||| ||| ||| ||  ||| ||  ||| ||| ||| |||
AAA GAC CTT TCA AAC CCC TCG AGA TAC TTG TGC
```

FIG. 31H

CODING SEGMENT C/D: (SEQ ID NO: 142 (bovine) and 178 (human))

```
Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn Val Pro
AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT GTG CCC      48
||| ||| ||| ||| ||| ||| ||| ||| ||  ||| ||| ||| ||| ||| ||| |||
AAG TGC CAA CCT GGA TTC ACT GGA GCA AGA TGT ACT GAG AAT GTG CCC

Met Lys Val Gln Thr Gln Glu
ATG AAA GTC CAA ACC CAA GAA                                      69
||| ||| ||| ||| | | ||| |||
ATG AAA GTC CAA AAC CAA GAA
          N
```

FIG. 31I

CODING SEGMENT D: (SEQ ID NO: 143 (bovine) and 179 (human))

```
Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met
AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG     48
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG

Ala Ser Phe Tyr
GCC AGC TTC TAC                                                  60
||| ||| ||| |||
GCC AGC TTC TAC
```

FIG. 31J

CODING SEGMENT D: (SEQ ID NO: 144 (bovine) and 180 (human))

```
Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu *
AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT GAA TAG                   36
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT GAA TAG
```

FIG. 31K

CODING SEGMENT D': (SEQ ID NO: 145 (bovine))

```
Lys His Leu Gly Ile Glu Phe Met Glu
AAG CAT CTT GGG ATT GAA TTT ATG GAG                              27
```

FIG. 31L

CODING SEGMENT H: (SEQ ID NO: 146 (bovine) and 181 (human))

```
Lys Ala Glu Glu Leu Tyr Gln Lys Arg Val Leu Thr Ile Thr Gly Ile
AAA GCG GAG GAG CTC TAC CAG AAG AGA GTG CTC ACC ATT ACC GGC ATT      48
AAG GCG GAG GAG CTG TAC CAG AAG AGA GTG CTG ACC ATA ACC GGC ATC

Cys Ile Ala Leu Leu Val Val Gly Ile Met Cys Val Val Val Tyr Cys
TGC ATC GCG CTG CTC GTG GTT GGC ATC ATG TGT GTG GTG GTC TAC TGC      96
TGC ATC GCC CTC CTT GTG GTC GGC ATC ATG TGT GTG GTG GCC TAC TGC
                                              A

Lys Thr Lys Lys Gln Arg Lys Lys Leu His Asp Arg Leu Arg Gln Ser
AAA ACC AAG AAA CAA CGG AAA AAG CTT CAT GAC CGG CTT CGG CAG AGC     144
AAA ACC AAG AAA CAG CGG AAA AAG CTG CAT GAC CGT CTT CGG CAG AGC

Leu Arg Ser Glu Arg Asn Thr Met Met Asn Val Ala Asn Gly Pro His
CTT CGG TCT GAA AGA AAC ACC ATG ATG AAC GTA GCC AAC GGG CCC CAC     192
CTT CGG TCT GAA CGA AAC AAT ATG ATG AAC ATT GCC AAT GGG CCT CAC
                          N                 I

His Pro Asn Pro Pro Pro Glu Asn Val Gln Leu Val Asn Gln Tyr Val
CAC CCC AAT CCG CCC CCC GAG AAC GTG CAG CTG GTG AAT CAA TAC GTA     240
CAT CCT AAC CCA CCC CCC GAG AAT GTC CAG CTG GTG AAT CAA TAC GTA

Ser Lys Asn Val Ile Ser Ser Glu His Ile Val Glu Arg Glu Ala Glu
TCT AAA AAT GTC ATC TCT AGC GAG CAT ATT GTT GAG AGA GAG GCG GAG     288
TCT AAA AAC GTC ATC TCC AGT GAG CAT ATT GTT GAG AGA GAA GCA GAG
```

FIG. 31M

```
Ser Ser Phe Ser Thr Ser His Tyr Thr Ser Thr Ala His His Ser Thr
AGC TCT TTT TCC ACC AGT CAC TAC ACT TCG ACA GCT CAT CAT TCC ACT      336
|   ||  ||| ||| ||| ||| ||| ||  ||| ||  ||| ||  ||| ||  ||| |||
ACA TCC TTT TCC ACC AGT CAC TAT ACT TCC ACA GCC CAT CAC TCC ACT
T

Thr Val Thr Gln Thr Pro Ser His Ser Trp Ser Asn Gly His Thr Glu
ACT GTC ACT CAG ACT CCC AGT CAC AGC TGG AGC AAT GGA CAC ACT GAA      384
||| ||| ||  ||| ||| ||  ||  ||| ||| ||| ||| ||  ||| ||| ||| |||
ACT GTC ACC CAG ACT CCT AGC CAC AGC TGG AGC AAC GGA CAC ACT GAA

Ser Ile Ile Ser Glu Ser His Ser Val Ile Val Met Ser Ser Val Glu
AGC ATC ATT TCG GAA AGC CAC TCT GTC ATC GTG ATG TCA TCC GTA GAA      432
|||  ||  ||  ||  ||| ||| ||| ||| ||  ||| ||| ||| ||| ||| ||| |||
AGC ATC CTT TCC GAA AGC CAC TCT GTA ATC GTG ATG TCA TCC GTA GAA
     L

Asn Ser Arg His Ser Ser Pro Thr Gly Gly Pro Arg Gly Arg Leu Asn
AAC AGT AGG CAC AGC AGC CCG ACT GGG GGC CCG AGA GGA CGT CTC AAT      480
||| ||| ||| ||| ||| ||| ||  ||| ||| ||| ||  ||| ||| ||| ||  |||
AAC AGT AGG CAC AGC AGC CCA ACT GGG GGC CCA AGA GGA CGT CTT AAT

Gly Leu Gly Gly Pro Arg Glu Cys Asn Ser Phe Leu Arg His Ala Arg
GGC TTG GGA GGC CCT CGT GAA TGT AAC AGC TTC CTC AGG CAT GCC AGA      528
|||    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
GGC ACA GGA GGC CCT CGT GAA TGT AAC AGC TTC CTC AGG CAT GCC AGA
    T

Glu Thr Pro Asp Ser Tyr Arg Asp Ser Pro His Ser Glu Arg
GAA ACC CCT GAC TCC TAC CGA GAC TCT CCT CAT AGT GAA AG              569
||| ||| ||| ||  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
GAA ACC CCT GAT TCC TAC CGA GAC TCT CCT CAT AGT GAA AG
```

FIG. 31N

CODING SEGMENT K: (SEQ ID NO: 161)

```
  A CAT AAC CTT ATA GCT GAG CTA AGG AGA AAC AAG GCC CAC AGA TCC        46
    His Asn Leu Ile Ala Glu Leu Arg Arg Asn Lys Ala His Arg Ser

AAA TGC ATG CAG ATC CAG CTT TCC GCA ACT CAT CTT AGA GCT TCT TCC        94
Lys Cys Met Gln Ile Gln Leu Ser Ala Thr His Leu Arg Ala Ser Ser

ATT CCC CAT TGG GCT TCA TTC TCT AAG ACC CCT TGG CCT TTA GGA AG       141
Ile Pro His Trp Ala Ser Phe Ser Lys Thr Pro Trp Pro Leu Gly Arg
```

FIG. 31O

CODING SEGMENT L: (SEQ ID NO: 147 (bovine) and 182 (human))

```
  Tyr Val Ser Ala Met Thr Thr Pro Ala Arg Met Ser Pro Val Asp
G TAT GTA TCA GCA ATG ACC ACC CCG GCT CGT ATG TCA CCT GTA GAT          46
| ||| ||  ||| ||  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
G TAT GTG TCA GCC ATG ACC ACC CCG GCT CGT ATG TCA CCT GTA GAT

Phe His Thr Pro Ser Ser Pro Lys Ser Pro Pro Ser Glu Met Ser Pro
TTC CAC ACG CCA AGC TCC CCC AAG TCA CCC CCT TCG GAA ATG TCC CCG        94
||| ||| ||| ||| ||| ||| ||| ||  ||  ||| ||| ||| ||| ||| ||  ||
TTC CAC ACG CCA AGC TCC CCC AAA TCG CCC CCT TCG GAA ATG TCT CCA

Pro Val Ser Ser Thr Thr Val Ser Met Pro Ser Met Ala Val Ser Pro
CCC GTG TCC AGC ACG ACG GTC TCC ATG CCC TCC ATG GCG GTC AGT CCC      142
||| ||| ||| ||| | | ||| ||  ||| ||| ||  ||| ||| ||| ||| ||  |||
CCC GTG TCC AGC ATG ACG GTG TCC ATG CCT TCC ATG GCG GTC AGC CCC
                M
Phe Val Glu Glu Glu Arg Pro Leu Leu Leu Val Thr Pro Pro Arg Leu
TTC GTG GAA GAG GAG AGA CCC CTG CTC CTT GTG ACG CCA CCA CGG CTG      190
|||  ||  ||| ||  ||| ||| ||  ||  ||  ||  ||| ||  ||| |||  ||  |||
TTC ATG GAA GAA GAG AGA CCT CTA CTT CTC GTG ACA CCA CCA AGG CTG
    N
Arg Glu Lys  -  Tyr Asp His His Ala Gln Gln Phe Asn Ser Phe His
CGG GAG AAG ... TAT GAC CAC CAC GCC CAG CAA TTC AAC TCG TTC CAC      238
|||  |||  |||     | |  |||  ||  |||  |  |||  ||  |||  | |  ||  |||  |||
CGG GAG AAG AAG TTT GAC CAT CAC CCT CAG CAG TTC AGC TCC TTC CAC
          K   F           P
Cys Asn Pro Ala His Glu Ser Asn Ser Leu Pro Pro Ser Pro Leu Arg
TGC AAC CCC GCG CAT GAG AGC AAC AGC CTG CCC CCC AGC CCC TTG AGG      286
  |  |||  |||  |||  |||  ||  ||  |||  |||  ||  ||   |  |||  |||  |||  |||
CAC AAC CCC GCG CAT GAC AGT AAC AGC CTC CCT GCT AGC CCC TTG AGG
N                   D                   A
```

FIG. 31P

```
Ile Val Glu Asp Glu Glu Tyr Glu Thr Thr Gln Glu Tyr Glu Pro Ala
ATA GTG GAG GAT GAG GAA TAT GAA ACG ACC CAG GAG TAC GAA CCA GCT      334
||| ||| ||| ||| ||| ||  ||| ||| ||| ||| ||  ||| ||| ||  ||| ||
ATA GTG GAG GAT GAG GAG TAT GAA ACG ACC CAA GAG TAC GAG CCA GCC

Gln Glu Pro Val Lys Lys Leu Thr Asn Ser Ser Arg Arg Ala Lys Arg
CAA GAG CCG GTT AAG AAA CTC ACC AAC AGC AGC CGG CGG GCC AAA AGA      382
||| ||| ||  ||| ||| ||| |||  || |||     ||| ||| ||| ||| ||| |||
CAA GAG CCT GTT AAG AAA CTC GCC AA. ..T AGC CGG CGG GCC AAA AGA
                            A

Thr Lys Pro Asn Gly His Ile Ala His Arg Leu Glu Met Asp Asn Asn
ACC AAG CCC AAT GGT CAC ATT GCC CAC AGG TTG GAA ATG GAC AAC AAC      430
||| ||| ||| ||| ||  ||| ||| ||   ||  ||  ||| |||  ||  ||| | | |||
ACC AAG CCC AAT GGC CAC ATT GCT AAC AGA TTG GAA GTG GAC AGC AAC
                              N           V       S

Thr Gly Ala Asp Ser Ser Asn Ser Glu Ser Glu Thr Glu Asp Glu Arg
ACA GGC GCT GAC AGC AGT AAC TCA GAG AGC GAA ACA GAG GAT GAA AGA      478
|||  ||  |   |  ||| ||| ||| ||| ||| ||  ||| |||  ||  ||| ||| |||
ACA AGC TCC CAG AGC AGT AAC TCA GAG AGT GAA ACA GAA GAT GAA AGA
    S   S   Q
```

FIG. 31Q

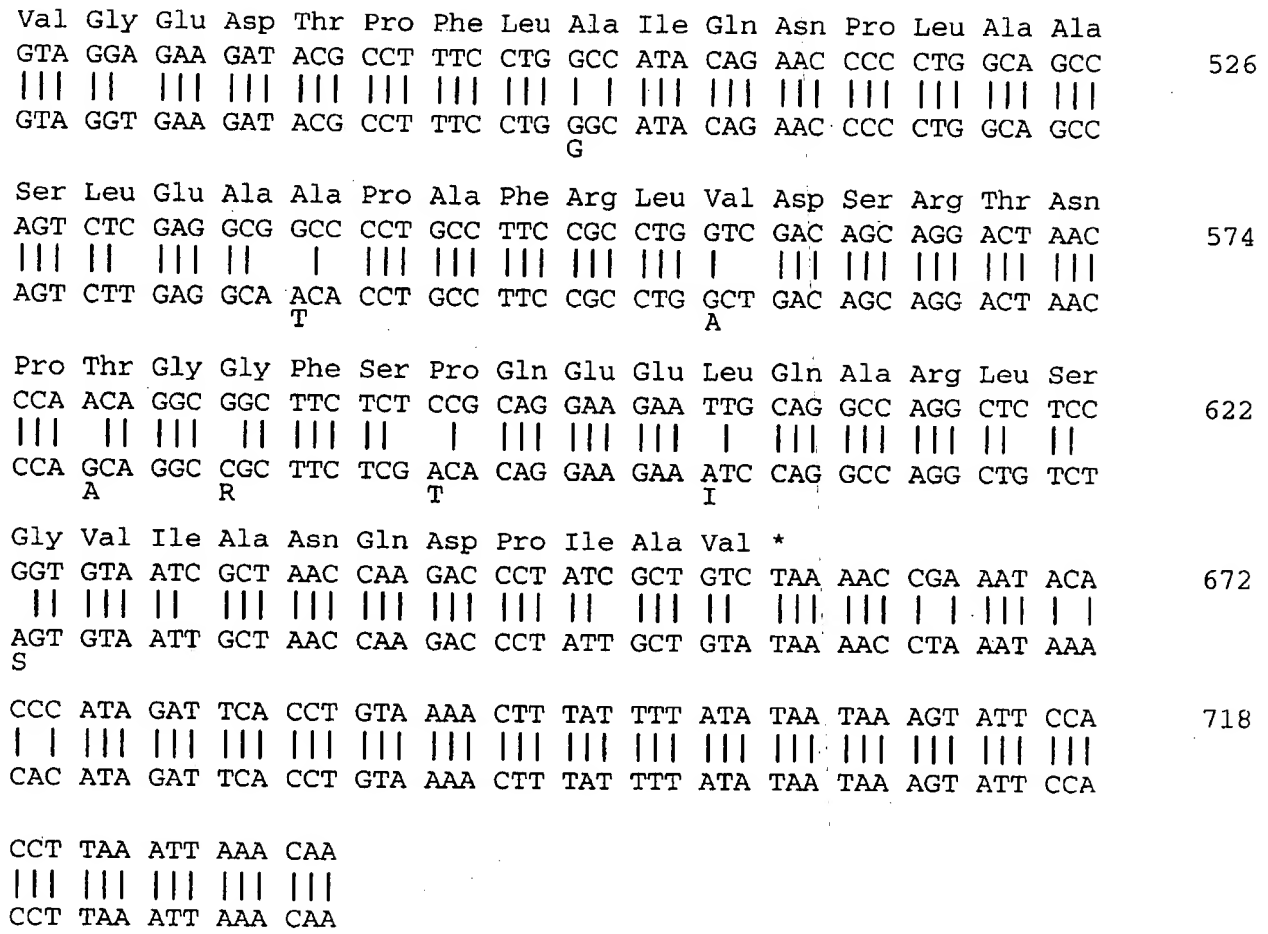

Val Gly Glu Asp Thr Pro Phe Leu Ala Ile Gln Asn Pro Leu Ala Ala
GTA GGA GAA GAT ACG CCT TTC CTG GCC ATA CAG AAC CCC CTG GCA GCC
526
GTA GGT GAA GAT ACG CCT TTC CTG GGC ATA CAG AAC CCC CTG GCA GCC
G
Ser Leu Glu Ala Ala Pro Ala Phe Arg Leu Val Asp Ser Arg Thr Asn
AGT CTC GAG GCG GCC CCT GCC TTC CGC CTG GTC GAC AGC AGG ACT AAC
574
AGT CTT GAG GCA ACA CCT GCC TTC CGC CTG GCT GAC AGC AGG ACT AAC
T
A
Pro Thr Gly Gly Phe Ser Pro Gln Glu Glu Leu Gln Ala Arg Leu Ser
CCA ACA GGC GGC TTC TCT CCG CAG GAA GAA TTG CAG GCC AGG CTC TCC
622
CCA GCA GGC CGC TTC TCG ACA CAG GAA GAA ATC CAG GCC AGG CTG TCT
A
R
T
I
Gly Val Ile Ala Asn Gln Asp Pro Ile Ala Val *
GGT GTA ATC GCT AAC CAA GAC CCT ATC GCT GTC TAA AAC CGA AAT ACA
672
AGT GTA ATT GCT AAC CAA GAC CCT ATT GCT GTA TAA AAC CTA AAT AAA
S
CCC ATA GAT TCA CCT GTA AAA CTT TAT TTT ATA TAA TAA AGT ATT CCA
718
CAC ATA GAT TCA CCT GTA AAA CTT TAT TTT ATA TAA TAA AGT ATT CCA
CCT TAA ATT AAA CAA
CCT TAA ATT AAA CAA

FIG. 31R

HUMAN CODING SEGMENT E:
(SEQ ID NO: 163)

```
ATG AGA TGG CGA CGC GCC CCG CGC CGC TCC GGG CGT CCC GGC CCC CGG  48
Met Arg Trp Arg Arg Ala Pro Arg Arg Ser Gly Arg Pro Gly Pro Arg

GCC CAG CGC CCC GGC TCC GCC GCC CGC TCG TCG CCG CCG CTG CCG CTG  96
Ala Gln Arg Pro Gly Ser Ala Ala Arg Ser Ser Pro Pro Leu Pro Leu

CTG CCA CTA CTG CTG CTG CTG GGG ACC GCG GCC CTG GCG CCG GGG GCG 144
Leu Pro Leu Leu Leu Leu Leu Gly Thr Ala Ala Leu Ala Pro Gly Ala

GCG GCC GGC AAC GAG GCG GCT CCC GCG GGG GCC TCG GTG TGC TAC TCG 192
Ala Ala Gly Asn Glu Ala Ala Pro Ala Gly Ala Ser Val Cys Tyr Ser

TCC CCG CCC AGC GTG GGA TCG GTG CAG GAG CTA GCT CAG CGC GCC GCG 240
Ser Pro Pro Ser Val Gly Ser Val Gln Glu Leu Ala Gln Arg Ala Ala

GTG GTG ATC GAG GGA AAG GTG CAC CCG CAG CGG CGG CAG CAG GGG GCA 288
Val Val Ile Glu Gly Lys Val His Pro Gln Arg Arg Gln Gln Gly Ala

CTC GAC AGG AAG GCG GCG GCG GCG GCG GGC GAG GCA GGG GCG TGG GGC 336
Leu Asp Arg Lys Ala Ala Ala Ala Ala Gly Glu Ala Gly Ala Trp Gly

GGC GAT CGC GAG CCG CCA GCC GCG GGC CCA CGG GCG CTG GGG CCG CCC 384
Gly Asp Arg Glu Pro Pro Ala Ala Gly Pro Arg Ala Leu Gly Pro Pro

GCC GAG GAG CCG CTG CTC GCC GCC AAC GGG ACC GTG CCC TCT TGG CCC 432
Ala Glu Glu Pro Leu Leu Ala Ala Asn Gly Thr Val Pro Ser Trp Pro

ACC GCC CCG GTG CCC AGC GCC GGC GAG CCC GGG GAG GAG GCG CCC TAT 480
Thr Ala Pro Val Pro Ser Ala Gly Glu Pro Gly Glu Glu Ala Pro Tyr

CTG GTG AAG GTG CAC CAG GTG TGG GCG GTG AAA GCC GGG GGC TTG AAG 528
Leu Val Lys Val His Gln Val Trp Ala Val Lys Ala Gly Gly Leu Lys

AAG GAC TCG CTG CTC ACC GTG CGC CTG GGG ACC TGG GGC CAC CCC GCC 576
Lys Asp Ser Leu Leu Thr Val Arg Leu Gly Thr Trp Gly His Pro Ala

TTC CCC TCC TGC GGG AGG CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC 624
Phe Pro Ser Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe

ATG GAG CCC GAC GCC AAC AGC ACC AGC CGC GCG CCG GCC GCC TTC CGA 672
Met Glu Pro Asp Ala Asn Ser Thr Ser Arg Ala Pro Ala Ala Phe Arg

GCC TCT TTC CCC CCT CTG GAG ACG GGC CGG AAC CTC AAG AAG GAG GTC 720
Ala Ser Phe Pro Pro Leu Glu Thr Gly Arg Asn Leu Lys Lys Glu Val

AGC CGG GTG CTG TGC AAG CGG TGC G                               745
Ser Arg Val Leu Cys Lys Arg Cys
```

FIG. 32A

GGF2BPP5 Nucleotide Sequence & Deduced Protein Sequence

SEQ ID NO: 148:

```
AGTTTCCCCC CCCAACTTGT CGGAACTCTG GGCTCGCGCG CAGGGCAGGA GCGGAGCGGC      60

GGCGGCTGCC CAGGCGATGC GAGCGCGGGC CGGACGGTAA TCGCCTCTCC CTCCTCGGGC     120

TGCGAGCGCG CCGGACCGAG GCAGCGACAG GAGCGGACCG CGGCGGGAAC CGAGGACTCC     180

CCAGCGGCGC GCCAGCAGGA GCCACCCCGC GAGCGTGCGA CCGGGACGGA GCGCCCGCCA     240

GTCCCAGGTG GCCCGGACCG CACGTTGCGT CCCCGCGCTC CCCGCCGGCG ACAGGAGACG     300

CTCCCCCCCA CGCCGCGCGC GCCTCGGCCC GGTCGCTGGC CCGCCTCCAC TCCGGGGACA     360

AACTTTTCCC GAAGCCGATC CCAGCCCTCG GACCCAAACT TGTCGCGCGT CGCCTTCGCC     420

GGGAGCCGTC CGCGCAGAGC GTGCACTTCT CGGGCGAG ATG TCG GAG CGC AGA          475
                                          Met Ser Glu Arg Arg

GAA GGC AAA GGC AAG GGG AAG GGC GGC AAG AAG GAC CGA GGC TCC GGG        523
Glu Gly Lys Gly Lys Gly Lys Gly Gly Lys Lys Asp Arg Gly Ser Gly

AAG AAG CCC GTG CCC GCG GCT GGC GGC CCG AGC CCA GCC TTG CCT CCC        571
Lys Lys Pro Val Pro Ala Ala Gly Gly Pro Ser Pro Ala Leu Pro Pro
CGC TTG AAA GAG ATG AAG ATG CAG GAG TCT GTG GCA GGT TCC AAA CTA        619
Arg Leu Lys Glu Met Lys Ser Gln Glu Ser Val Ala Gly Ser Lys Leu

GTG CTT CGG TGC GAG ACC AGT TCT GAA TAC TCC TCT CTC AAG TTC AAG        667
Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu Lys Phe Lys

TGG TTC AAG AAT GGG AGT GAA TTA AGC CGA AAG AAC AAA CCA CAA AAC        715
Trp Phe Lys Asn Gly Ser Glu Leu Ser Arg Lys Asn Lys Pro Gln Asn

ATC AAG ATA CAG AAA AGG CCG GGG AAG TCA GAA CTT CGC ATT AGC AAA        763
Ile Lys Ile Gln Lys Arg Pro Gly Lys Ser Glu Leu Arg Ile Ser Lys

GCG TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC AGC AAA        811
Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys
```

FIG. 32B

GGF2BPP5 Nucleotide Sequence & Deduced Protein Sequence

```
CTA GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG TCA AAC      859
Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn

GAG ATC ACC ACT GGC ATG CCA GCC TCA ACT GAG ACA GCG TAT GTG TCT      907
Glu Ile Thr Thr Gly Met Pro Ala Ser Thr Glu Thr Ala Tyr Val Ser

TCA GAG TCT CCC ATT AGA ATA TCA GTA TCA ACA GAA GGA ACA AAT ACT      955
Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Thr Asn Thr

TCT TCA TCC ACA TCC ACA TCT ACA GCT GGG ACA AGC CAT CTT GTC AAG     1003
Ser Ser Ser Thr Ser Thr Ser Thr Ala Gly Thr Ser His Leu Val Lys

TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGC GAG TGC TTC     1051
Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys Phe

ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC TTG TGC AAG TGC CCA     1099
Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys Pro

AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC     1147
Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe

TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT GAA TAGGCGCATG          1193
Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu

CTCAGTCGGT GCCGCTTTCT TGTTGCCGCA TCTCCCCTCA GATTCAACCT AGAGCTAGAT   1253

GCGTTTTACC AGGTCTAACA TTGACTGCCT CTGCCTGTCG CATGAGAACA TTAACACAAG   1313

CGATTGTATG ACTTCCTCTG TCCGTGACTA GTGGGCTCTG AGCTACTCGT AGGTGCGTAA   1373

GGCTCCAGTG TTTCTGAAAT TGATCTTGAA TTACTGTGAT ACGACATGAT AGTCCCTCTC   1433

ACCCAGTGCA ATGACAATAA AGGCCTTGAA AAGTCTCACT TTTATTGAGA AAATAAAAAT   1493

CGTTCCACGG GACAGTCCCT CTTCTTTATA AAATGACCCT ATCCTTGAAA AGGAGGTGTG   1553

TTAAGTTGTA ACCAGTACAC ACTTGAAATG ATGGTAAGTT CGCTTCGGTT CAGAATGTGT   1613

TCTTTCTGAC AAATAAACAG AATAAAAAAA AAAAAAAAAA A                       1654
```

FIG. 33A

GGF2BPP2 Nucleotide Sequence & Deduced Protein Sequence

SEQ ID NO: 149:

```
CAT CAN GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG      48
His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu

CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC TGC      96
Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys

GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAG     144
Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu

GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT CCC CCC     192
Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro

TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT GTG     240
Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala Val

CAA CGG TGC GCC TTG CCT CCC CGC TTG AAA GAG ATG AAG AGT CAG GAG     288
Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu

TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA     336
Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu

TAC TCC TCT CTC AAG TTC AAG TGG TTC AAG AAT GGG AGT GAA TTA AGC     384
Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser

CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG GGG AAG     432
Arg Lys Asn Lys Pro Glu Asn Ile Lys Ile Gln Lys Arg Pro Gly Lys

TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT     480
Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr

ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC     528
Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn
```

FIG. 33B

GGF2BPP2 Nucleotide Sequence & Deduced Protein Sequence

```
ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG ACA      576
Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly Thr

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT      624
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC      672
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr

TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT      720
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn

GTG CCC ATG AAA GTC CAA ACC CAA GAA AAG TGC CCA AAT GAG TTT ACT      768
Val Pro Met Lys Val Gln Thr Gln Glu Lys Cys Pro Asn Glu Phe Thr

GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC AGT ACG TCC      816
Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Ser Thr Ser

ACT CCC TTT CTG TCT CTG CCT GAA TAGCGCATCT CAGTCGGTGC CGCTTTCTTG     870
Thr Pro Phe Leu Ser Leu Pro Glu

TTGCCGCATC TCCCCTCAGA TTCCNCCTAG AGCTAGATGC GTTTTACCAG GTCTAACATT    930

GACTGCCTCT GCCTGTCGCA TGAGAACATT AACACAAGCG ATTGTATGAC TTCCTCTGTC    990

CGTGACTAGT GGGCTCTGAG CTACTCGTAG GTGCGTAAGG CTCCAGTGTT TCTGAAATTG   1050

ATCTTGAATT ACTGTGATAC GACATGATAG TCCCTCTCAC CCAGTGCAAT GACAATAAAG   1110

GCCTTGAAAA GTCAAAAAAA AAAAAAAAAA                                    1140
```

FIG. 34A

GGF2BPP4 Nucleotide Sequence & Deduced Protein Sequence

SEQ ID NO: 150:

```
G AAG TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA      49
  Lys Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu

TAT ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC      97
Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala

AAC ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG     145
Asn Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly

ACA AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG     193
Thr Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val

AAT GGA GGC GAC TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA     241
Asn Gly Gly Asp Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg

TAC TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG     289
Tyr Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu

AAT GTG CCC ATG AAA GTC CAA ACC CAA GAA AAA GCG GAG GAG CTC TAC     337
Asn Val Pro Met Lys Val Gln Thr Gln Glu Lys Ala Glu Glu Leu Tyr

CAG AAG AGA GTG CTC ACC ATT ACC GGC ATT TGC ATC GCG CTG CTC GTG     385
Gln Lys Arg Val Leu Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu Val

GTT GGC ATC ATG TGT GTG GTG GTC TAC TGC AAA ACC AAG AAA CAA CGG     433
Val Gly Ile Met Cys Val Val Val Tyr Cys Lys Thr Lys Lys Gln Arg

AAA AAG CTT CAT GAC CGG CTT CGG CAG AGC CTT CGG TCT GAA AGA AAC     481
Lys Lys Leu His Asp Arg Leu Arg Gln Ser Leu Arg Ser Glu Arg Asn

ACC ATG ATG AAC GTA GCC AAC GGG CCC CAC CAC CCC AAT CCG CCC CCC     529
Thr Met Met Asn Val Ala Asn Gly Pro His His Pro Asn Pro Pro Pro

GAG AAC GTG CAG CTG GTG AAT CAA TAC GTA TCT AAA AAT GTC ATC TCT     577
Glu Asn Val Gln Leu Val Asn Gln Tyr Val Ser Lys Asn Val Ile Ser
```

FIG. 34B

GGF2BPP4 Nucleotide Sequence & Deduced Protein Sequence

```
AGC GAG CAT ATT GTT GAG AGA GAG GCG GAG AGC TCT TTT TCC ACC AGT          625
Ser Glu His Ile Val Glu Arg Glu Ala Glu Ser Ser Phe Ser Thr Ser

CAC TAC ACT TCG ACA GCT CAT CAT TCC ACT ACT GTC ACT CAG ACT CCC          673
His Tyr Thr Ser Thr Ala His His Ser Thr Thr Val Thr Gln Thr Pro

AGT CAC AGC TGG AGC AAT GGA CAC ACT GAA AGC ATC ATT TCG GAA AGC          721
Ser His Ser Trp Ser Asn Gly His Thr Glu Ser Ile Ile Ser Glu Ser

CAC TCT GTC ATC GTG ATG TCA TCC GTA GAA AAC AGT AGG CAC AGC AGC          769
His Ser Val Ile Val Met Ser Ser Val Glu Asn Ser Arg His Ser Ser

CCG ACT GGG GGC CCG AGA GGA CGT CTC AAT GGC TTG GGA GGC CCT CGT          817
Pro Thr Gly Gly Pro Arg Gly Arg Leu Asn Gly Leu Gly Gly Pro Arg

GAA TGT AAC AGC TTC CTC AGG CAT GCC AGA GAA ACC CCT GAC TCC TAC          865
Glu Cys Asn Ser Phe Leu Arg His Ala Arg Glu Thr Pro Asp Ser Tyr

CGA GAC TCT CCT CAT AGT GAA AGA CAT AAC CTT ATA GCT GAG CTA AGG          913
Arg Asp Ser Pro His Ser Glu Arg His Asn Leu Ile Ala Glu Leu Arg

AGA AAC AAG GCC CAC AGA TCC AAA TGC ATG CAG ATC CAG CTT TCC GCA          961
Arg Asn Lys Ala His Arg Ser Lys Cys Met Gln Ile Gln Leu Ser Ala

ACT CAT CTT AGA GCT TCT TCC ATT CCC CAT TGG GCT TCA TTC TCT AAG         1009
Thr His Leu Arg Ala Ser Ser Ile Pro His Trp Ala Ser Phe Ser Lys

ACC CCT TGG CCT TTA GGA AGG TAT GTA TCA GCA ATG ACC ACC CCG GCT         1057
Thr Pro Trp Pro Leu Gly Arg Tyr Val Ser Ala Met Thr Thr Pro Ala

CGT ATG TCA CCT GTA GAT TTC CAC ACG CCA AGC TCC CCC AAG TCA CCC         1105
Arg Met Ser Pro Val Asp Phe His Thr Pro Ser Ser Pro Lys Ser Pro

CCT TCG GAA ATG TCC CCG CCC GTG TCC AGC ACG ACG GTC TCC ATG CCC         1153
Pro Ser Glu Met Ser Pro Pro Val Ser Ser Thr Thr Val Ser Met Pro
```

FIG. 34C

GGF2BPP4 Nucleotide Sequence & Deduced Protein Sequence

```
TCC ATG GCG GTC AGT CCC TTC GTG GAA GAG GAG AGA CCC CTG CTC CTT      1201
Ser Met Ala Val Ser Pro Phe Val Glu Glu Glu Arg Pro Leu Leu Leu

GTG ACG CCA CCA CGG CTG CGG GAG AAG TAT GAC CAC CAC GCC CAG CAA      1249
Val Thr Pro Pro Arg Leu Arg Glu Lys Tyr Asp His His Ala Gln Gln

TTC AAC TCG TTC CAC TGC AAC CCC GCG CAT GAG AGC AAC AGC CTG CCC      1297
Phe Asn Ser Phe His Cys Asn Pro Ala His Glu Ser Asn Ser Leu Pro

CCC AGC CCC TTG AGG ATA GTG GAG GAT GAG GAA TAT GAA ACG ACC CAG      1345
Pro Ser Pro Leu Arg Ile Val Glu Asp Glu Glu Tyr Glu Thr Thr Gln

GAG TAC GAA CCA GCT CAA GAG CCG GTT AAG AAA CTC ACC AAC AGC AGC      1393
Glu Tyr Glu Pro Ala Gln Glu Pro Val Lys Lys Leu Thr Asn Ser Ser

CGG CGG GCC AAA AGA ACC AAG CCC AAT GGT CAC ATT GCC CAC AGG TTG      1441
Arg Arg Ala Lys Arg Thr Lys Pro Asn Gly His Ile Ala His Arg Leu

GAA ATG GAC AAC AAC ACA GGC GCT GAC AGC AGT AAC TCA GAG AGC GAA      1489
Glu Met Asp Asn Asn Thr Gly Ala Asp Ser Ser Asn Ser Glu Ser Glu

ACA GAG GAT GAA AGA GTA GGA GAA GAT ACG CCT TTC CTG GCC ATA CAG      1537
Thr Glu Asp Glu Arg Val Gly Glu Asp Thr Pro Phe Leu Ala Ile Gln

AAC CCC CTG GCA GCC AGT CTC GAG GCG GCC CCT GCC TTC CGC CTG GTC      1585
Asn Pro Leu Ala Ala Ser Leu Glu Ala Ala Pro Ala Phe Arg Leu Val

GAC AGC AGG ACT AAC CCA ACA GGC GGC TTC TCT CCG CAG GAA GAA TTG      1633
Asp Ser Arg Thr Asn Pro Thr Gly Gly Phe Ser Pro Gln Glu Glu Leu

CAG GCC AGG CTC TCC GGT GTA ATC GCT AAC CAA GAC CCT ATC GCT GTC      1681
Gln Ala Arg Leu Ser Gly Val Ile Ala Asn Gln Asp Pro Ile Ala Val

TAAAACCGAA ATACACCCAT AGATTCACCT GTAAAACTTT ATTTTATATA ATAAAGTATT    1741

CCACCTTAAA TTAAACAAAA AAA                                           1764
```

FIG. 35

```
                                    *           *               * *         *
GGF2bpp5 (SEQ ID NO: 151) KCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFY
GGF2bpp4 (SEQ ID NO: 152) KCAEKEKTFCVNGGDCFMVKDLSNPSRYLCKCQPGFTGARCTENVPMKVQ
hEGF     (SEQ ID NO: 153) ECLRKYKDFCIH-GECKYVKELRAPS---CKCQQEYFGERCGEKSNKTHS
```

FIG. 36

200 kDa Tyrosine Phosphorylation Compared with Mitogenic Activity

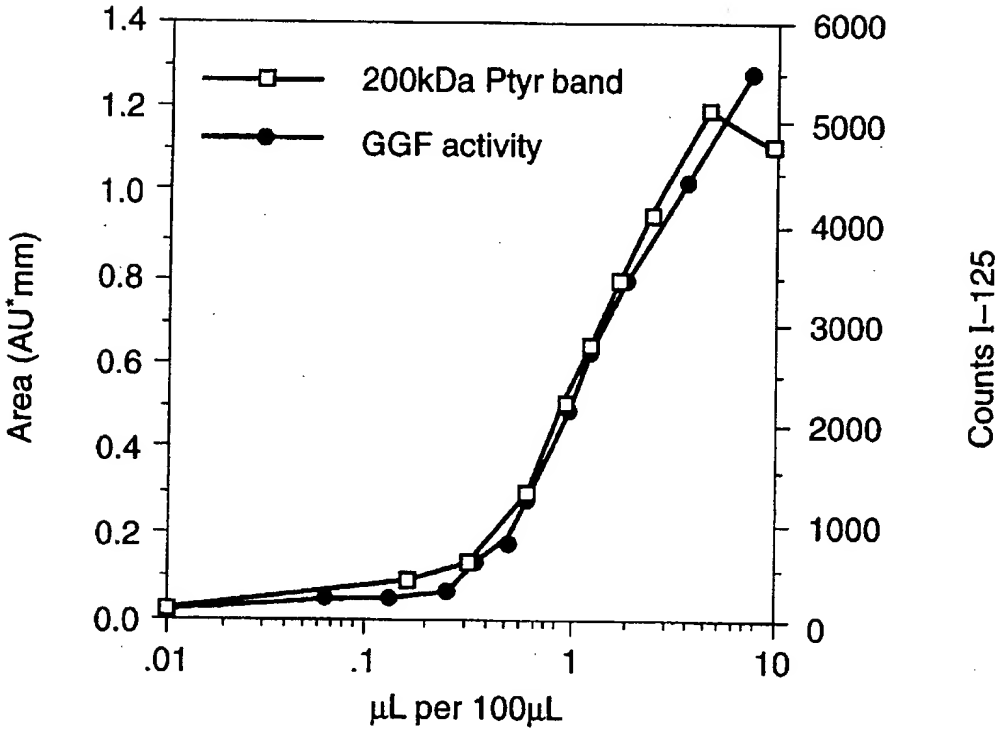


FIG. 37A GGF/Heregulin Splicing Variants

F-B-A'	F-E-B-A'
F-B-A-C-C/D-D	F-E-B-A-C-C/D-D
F-B-A-C-C/D-H	F-E-B-A-C-C/D-H
F-B-A-C-C/D-H-L	F-E-B-A-C-C/D-H-L
F-B-A-C-C/D-H-K-L	F-E-B-A-C-C/D-H-K-L
F-B-A-C-C/D-D'-H	F-E-B-A-C-C/D-D'-H
F-B-A-C-C/D-D'-H-L	F-E-B-A-C-C/D-D'-H-L
F-B-A-C-C/D-D'-H-K-L	F-E-B-A-C-C/D-D'-H-K-L
F-B-A-C-C/D'-D	F-E-B-A-C-C/D'-D
F-B-A-C-C/D'-H	F-E-B-A-C-C/D'-H
F-B-A-C-C/D'-H-L	F-E-B-A-C-C/D'-H-L
F-B-A-C-C/D'-H-K-L	F-E-B-A-C-C/D'-H-K-L
F-B-A-C-C/D'-D'-H	F-E-B-A-C-C/D'-D'-H
F-B-A-C-C/D'-D'-H-L	F-E-B-A-C-C/D'-D'-H-L
F-B-A-C-C/D'-D'-H-K-L	F-E-B-A-C-C/D'-D'-H-K-L
F-B-A-C-C/D-C/D'-D	F-E-B-A-C-C/D-C/D'-D
F-B-A-C-C/D-C/D'-H	F-E-B-A-C-C/D-C/D'-H
F-B-A-C-C/D-C/D'-H-L	F-E-B-A-C-C/D-C/D'-H-L
F-B-A-C-C/D-C/D'-H-K-L	F-E-B-A-C-C/D-C/D'-H-K-L
F-B-A-C-C/D-C/D'-D'-H	F-E-B-A-C-C/D-C/D'-D'-H
F-B-A-C-C/D-C/D'-D'-H-L	F-E-B-A-C-C/D-C/D'-D'-H-L
F-B-A-C-C/D-C/D'-D'-H-K-L	F-E-B-A-C-C/D-C/D'-D'-H-K-L
F-B-A-G-C-C/D-D	F-E-B-A-G-C-C/D-D
F-B-A-G-C-C/D-H	F-E-B-A-G-C-C/D-H
F-B-A-G-C-C/D-H-L	F-E-B-A-G-C-C/D-H-L
F-B-A-G-C-C/D-H-K-L	F-E-B-A-G-C-C/D-H-K-L
F-B-A-G-C-C/D-D'-H	F-E-B-A-G-C-C/D-D'-H
F-B-A-G-C-C/D-D'-H-L	F-E-B-A-G-C-C/D-D'-H-L
F-B-A-G-C-C/D-D'-H-K-L	F-E-B-A-G-C-C/D-D'-H-K-L
F-B-A-G-C-C/D'-D	F-E-B-A-G-C-C/D'-D
F-B-A-G-C-C/D'-H	F-E-B-A-G-C-C/D'-H
F-B-A-G-C-C/D'-H-L	F-E-B-A-G-C-C/D'-H-L
F-B-A-G-C-C/D'-H-K-L	F-E-B-A-G-C-C/D'-H-K-L
F-B-A-G-C-C/D'-D'-H	F-E-B-A-G-C-C/D'-D'-H
F-B-A-G-C-C/D'-D'-H-L	F-E-B-A-G-C-C/D'-D'-H-L
F-B-A-G-C-C/D'-D'-H-K-L	F-E-B-A-G-C-C/D'-D'-H-K-L
F-B-A-G-C-C/D-C/D'-D	F-E-B-A-G-C-C/D-C/D'-D
F-B-A-G-C-C/D-C/D'-H	F-E-B-A-G-C-C/D-C/D'-H
F-B-A-G-C-C/D-C/D'-H-L	F-E-B-A-G-C-C/D-C/D'-H-L
F-B-A-G-C-C/D-C/D'-H-K-L	F-E-B-A-G-C-C/D-C/D'-H-K-L
F-B-A-G-C-C/D-C/D'-D'-H	F-E-B-A-G-C-C/D-C/D'-D'-H
F-B-A-G-C-C/D-C/D'-D'-H-L	F-E-B-A-G-C-C/D-C/D'-D'-H-L
F-B-A-G-C-C/D-C/D'-D'-H-K-L	F-E-B-A-G-C-C/D-C/D'-D'-H-K-L

FIG. 37B

GGF/Heregulin Splicing Variants

E-B-A'

E-B-A-C-C/D-D
E-B-A-C-C/D-H
E-B-A-C-C/D-H-L
E-B-A-C-C/D-H-K-L
E-B-A-C-C/D-D'-H
E-B-A-C-C/D-D'-H-L
E-B-A-C-C/D-D'-H-K-L
E-B-A-C-C/D'-D
E-B-A-C-C/D'-H
E-B-A-C-C/D'-H-L
E-B-A-C-C/D'-H-K-L
E-B-A-C-C/D'-D'-H
E-B-A-C-C/D'-D'-H-L
E-B-A-C-C/D'-D'-H-K-L
E-B-A-C-C/D-C/D'-D
E-B-A-C-C/D-C/D'-H
E-B-A-C-C/D-C/D'-H-L
E-B-A-C-C/D-C/D'-H-K-L
E-B-A-C-C/D-C/D'-D'-H
E-B-A-C-C/D-C/D'-D'-H-L
E-B-A-C-C/D-C/D'-D'-H-K-L

E-B-A-G-C-C/D-D
E-B-A-G-C-C/D-H
E-B-A-G-C-C/D-H-L
E-B-A-G-C-C/D-H-K-L
E-B-A-G-C-C/D-D'-H
E-B-A-G-C-C/D-D'-H-L
E-B-A-G-C-C/D-D'-H-K-L
E-B-A-G-C-C/D'-D
E-B-A-G-C-C/D'-H
E-B-A-G-C-C/D'-H-L
E-B-A-G-C-C/D'-H-K-L
E-B-A-G-C-C/D'-D'-H
E-B-A-G-C-C/D'-D'-H-L
E-B-A-G-C-C/D'-D'-H-K-L
E-B-A-G-C-C/D-C/D'-D
E-B-A-G-C-C/D-C/D'-H
E-B-A-G-C-C/D-C/D'-H-L
E-B-A-G-C-C/D-C/D'-H-K-L
E-B-A-G-C-C/D-C/D'-D'-H
E-B-A-G-C-C/D-C/D'-D'-H-L
E-B-A-G-C-C/D-C/D'-D'-H-K-L

FIG. 38

EGFL1

SEQ ID NO: 154:

```
AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT    48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC    96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr

TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC   144
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr

GTA ATG GCC AGC TTC TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT   192
Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro

GAA TAG                                                          198
Glu
```

FIG. 39

EGFL2

SEQ ID NO: 155:

```
AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT     48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC     96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr

TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT    144
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn

GTG CCC ATG AAA GTC CAA ACC CAA GAA AAA GCG GAG GAG CTC TAC TAA    192
Val Pro Met Lys Val Gln Thr Gln Glu Lys Ala Glu Glu Leu Tyr
```

FIG. 40

EGFL3

SEQ ID NO: 156:

```
AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT   48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC   96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr

TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC  144
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr

GTA ATG GCC AGC TTC TAC AAA GCG GAG GAG CTC TAC TAA              183
Val Met Ala Ser Phe Tyr Lys Ala Glu Glu Leu Tyr
```

FIG. 41

EGFL4

SEQ ID NO: 157:

```
AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT     48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC     96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr

TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC    144
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr

GTA ATG GCC AGC TTC TAC AAG CAT CTT GGG ATT GAA TTT ATG GAG AAA    192
Val Met Ala Ser Phe Tyr Lys His Leu Gly Ile Glu Phe Met Glu Lys

GCG GAG GAG CTC TAC TAA                                            210
Ala Glu Glu Leu Tyr
```

FIG. 42

EGFL5

SEQ ID NO: 158:

```
AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT     48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC     96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr

TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT    144
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn

GTG CCC ATG AAA GTC CAA ACC CAA GAA AAG TGC CCA AAT GAG TTT ACT    192
Val Pro Met Lys Val Gln Thr Gln Glu Lys Cys Pro Asn Glu Phe Thr

GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC AGT ACG TCC    240
Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Ser Thr Ser

ACT CCC TTT CTG TCT CTG CCT GAA TAG                                267
Thr Pro Phe Leu Ser Leu Pro Glu
```

FIG. 43

EGFL6

SEQ ID NO: 159:

```
AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT     48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC     96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr

TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT    144
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn

GTG CCC ATG AAA GTC CAA ACC CAA GAA AAG TGC CCA AAT GAG TTT ACT    192
Val Pro Met Lys Val Gln Thr Gln Glu Lys Cys Pro Asn Glu Phe Thr

GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC AAA GCG GAG    240
Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Lys Ala Glu

GAG CTC TAC TAA                                                   252
Glu Leu Tyr
```

FIG. 44
GGF2HBS5

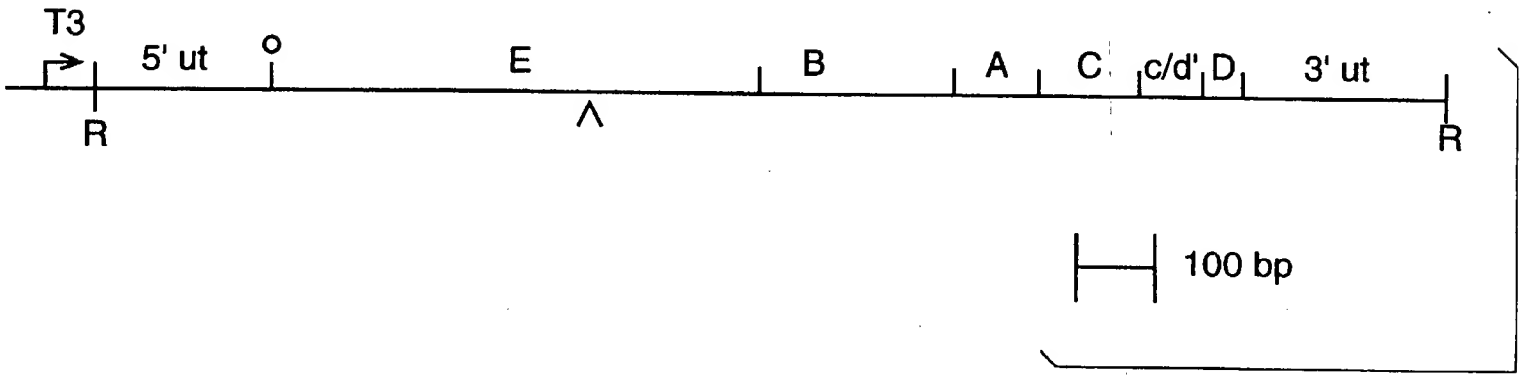


FIG. 45A

Nucleotide Sequence & Deduced Acid Sequence of GGF2HBS5

SEQ ID NO: 21:

```
GGAATTCCTT TTTTTTTTTT TTTTTTTCTT NNTTTTTTTT TGCCCTTATA CCTCTTCGCC          60

TTTCTGTGGT TCCATCCACT TCTTCCCCCT CCTCCTCCCA TAAACAACTC TCCTACCCCT         120

GCACCCCCAA TAAATAAATA AAAGGAGGAG GGCAAGGGGG GAGGAGGAGG AGTGGTGCTG         180

CGAGGGGAAG GAAAAGGGAG GCAGCGCGAG AAGAGCCGGG CAGAGTCCGA ACCGACAGCC         240

AGAAGCCCGC ACGCACCTCG CACC ATG AGA TGG CGA CGC GCC CCG CGC CGC              291
                           Met Arg Trp Arg Arg Ala Pro Arg Arg

TCC GGG CGT CCC GGC CCC CGG GCC CAG CGC CCC GGC TCC GCC GCC CGC            339
Ser Gly Arg Pro Gly Pro Arg Ala Gln Arg Pro Gly Ser Ala Ala Arg

TCG TCG CCG CCG CTG CCG CTG CTG CCA CTA CTG CTG CTG CTG GGG ACC            387
Ser Ser Pro Pro Leu Pro Leu Leu Pro Leu Leu Leu Leu Leu Gly Thr
                                        Val Cys Leu Leu Thr Val
                                                          GGF-II 09

GCG GCC CTG GCG CCG GGG GCG GCG GCC GGC AAC GAG GCG GCT CCC GCG            435
Ala Ala Leu Ala Pro Gly Ala Ala Ala Gly Asn Glu Ala Ala Pro Ala
Ala Ala Leu Pro Pro

GGG GCC TCG GTG TGC TAC TCG TCC CCG CCC AGC GTG GGA TCG GTG CAG            483
Gly Ala Ser Val Cys Tyr Ser Ser Pro Pro Ser Val Gly Ser Val Gln
                        Ala Ser Pro Val Ser Val Gly Ser Val Gln
                                                GGF-II 08

GAG CTA GCT CAG CGC|GCC GCG GTG GTG ATC GAG GGA AAG GTG CAC CCG            531
Glu Leu Ala Gln Arg|Ala Ala Val Val Ile Glu Gly Lys Val His Pro
Glu Leu Val Gln Arg|Trp Phe Val Val Ile Glu Gly Lys
                   |                 GGF-II 04
```

FIG. 45B

Nucleotide Sequence & Deduced Acid Sequence of GGF2HBS5

```
CAG CGG CGG CAG CAG GGG GCA CTC GAC AGG AAG GCG GCG GCG GCG GCG          579
Gln Arg Arg Gln Gln Gly Ala Leu Asp Arg Lys Ala Ala Ala Ala Ala

GGC GAG GCA GGG GCG TGG GGC GGC GAT CGC GAG CCG CCA GCC GCG GGC          627
Gly Glu Ala Gly Ala Trp Gly Gly Asp Arg Glu Pro Pro Ala Ala Gly

CCA CGG GCG CTG GGG CCG CCC GCC GAG GAG CCG CTG CTC GCC GCC AAC          675
Pro Arg Ala Leu Gly Pro Pro Ala Glu Glu Pro Leu Leu Ala Ala Asn

GGG ACC GTG CCC TCT TGG CCC ACC GCC CCG GTG CCC AGC GCC GGC GAG          723
Gly Thr Val Pro Ser Trp Pro Thr Ala Pro Val Pro Ser Ala Gly Glu

CCC GGG GAG GAG GCG CCC TAT CTG GTG AAG GTG CAC CAG GTG TGG GCG          771
Pro Gly Glu Glu Ala Pro Tyr Leu Val Lys Val His Gln Val Trp Ala
                                    Lys Val His Glu Val Trp Ala
                                         GGF-II 01 & GGF-II 11

GTG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG CTC ACC GTG CGC CTG          819
Val Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu Leu Thr Val Arg Leu
Ala Lys                         Asp Leu Leu Leu Xaa Val      Leu
                                      GGF-II 10

GGG ACC TGG GGC CAC CCC GCC TTC CCC TCC TGC GGG AGG CTC AAG GAG          867
Gly Thr Trp Gly His Pro Ala Phe Pro Ser Cys Gly Arg Leu Lys Glu
Gly Ala Trp Gly Pro Pro Ala Phe Pro Val Xaa Tyr
            GGF-II 03

GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAC GCC AAC AGC ACC AGC          915
Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Asp Ala Asn Ser Thr Ser
            Tyr Ile Phe Phe Met Glu Pro Gla Ala Xaa Ser Ser Gly
                                  GGF-II 02
```

FIG. 45C

Nucleotide Sequence & Deduced Acid Sequence of GGF2HBS5

```
CGC GCG CCG GCC GCC TTC CGA GCC TCT TTC CCC CCT CTG GAG ACG GGC          963
Arg Ala Pro Ala Ala Phe Arg Ala Ser Phe Pro Pro Leu Glu Thr Gly

CGG AAC CTC AAG AAG GAG GTC AGC CGG GTG CTG TGC AAG CGG TGC GCC         1011
Arg Asn Leu Lys Lys Glu Val Ser Arg Val Leu Cys Lys Arg Cys Ala

TTG CCT CCC CAA TTG AAA GAG ATG AAA AGC CAG GAA TCG GCT GCA GGT         1059
Leu Pro Pro Gln Leu Lys Glu Met Lys Ser Gln Glu Ser Ala Ala Gly

TCC AAA CTA GTC CTT CGG TGT GAA ACC AGT TCT GAA TAC TCC TCT CTC         1107
Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu
        Leu Val Leu Arg
           GGF-II 06

AGA TTC AAG TGG TTC AAG AAT GGG AAT GAA TTG AAT CGA AAA AAC AAA         1155
Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys Asn Lys

CCA CAA AAT ATC AAG ATA CAA AAA AAG CCA GGG AAG TCA GAA CTT CGC         1203
Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu Leu Arg

ATT AAC AAA GCA TCA CTG GCT GAT TCT GGA GAG TAT ATG TGC AAA GTG         1251
Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val
        Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Xaa Lyx
                              GGF-II 12

ATC AGC AAA TTA GGA AAT GAC AGT GCC TCT GCC AAT ATC ACC ATC GTG         1299
Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val

GAA TCA AAC GCT ACA TCT ACA TCC ACC ACT GGG ACA AGC CAT CTT GTA         1347
Glu Ser Asn Ala Thr Ser Thr Ser Thr Thr Gly Thr Ser His Leu Val
```

FIG. 45D

Nucleotide Sequence & Deduced Acid Sequence of GGF2HBS5

```
AAA TGT GCG GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGG GAG TGC          1395
Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys

TTC ATG GTG AAA GAC CTT TCA AAC CCC TCG AGA TAC TTG TGC AAG TGC          1443
Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys

CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC          1491
Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser

TTC TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT GAA                      1530
Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu

TAGGAGCATG CTCAGTTGGT GCTGCTTTCT TGTTGCTGCA TCTCCCCTCA GATTCCACCT       1590

AGAGCTAGAT GTGTCTTACC AGATCTAATA TTGACTGCCT CTGCCTGTCG CATGAGAACA       1650

TTAACAAAAG CAATTGTATT ACTTCCTCTG TTCGCGACTA GTTGGCTCTG AGATACTAAT       1710

AGGTGTGTGA GGCTCCGGAT GTTTCTGGAA TTGATATTGA ATGATGTGAT ACAAATTGAT       1770

AGTCAATATC AAGCAGTGAA ATATGATAAT AAAGGCATTT CAAAGTCTCA CTTTTATTGA       1830

TAAAATAAAA ATCATTCTAC TGAACAGTCC ATCTTCTTTA TACAATGACC ACATCCTGAA       1890

AAGGGTGTTG CTAAGCTGTA ACCGATATGC ACTTGAAATG ATGGTAAGTT AATTTTGATT       1950

CAGAATGTGT TATTTGTCAC AAATAAACAT AATAAAAGGA AAAAAAAAAA AAA              2003
```

FIG. 46

Schwann Cell Proliferation Assay

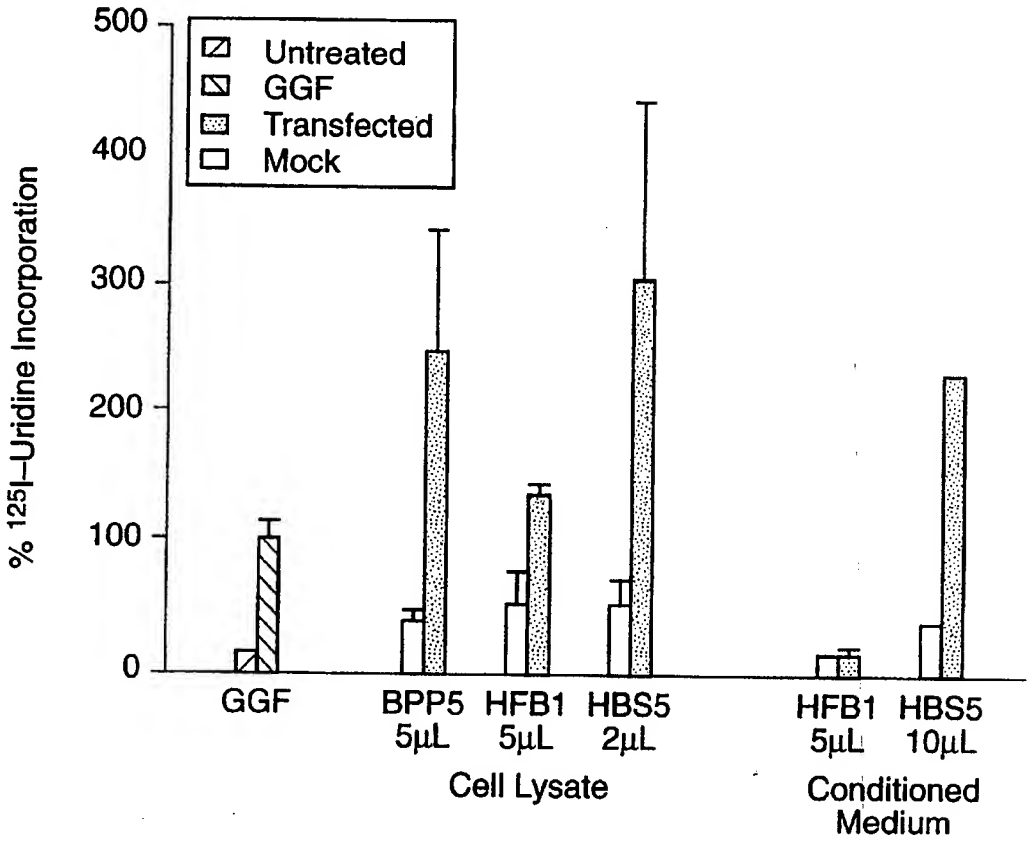


FIG. 47

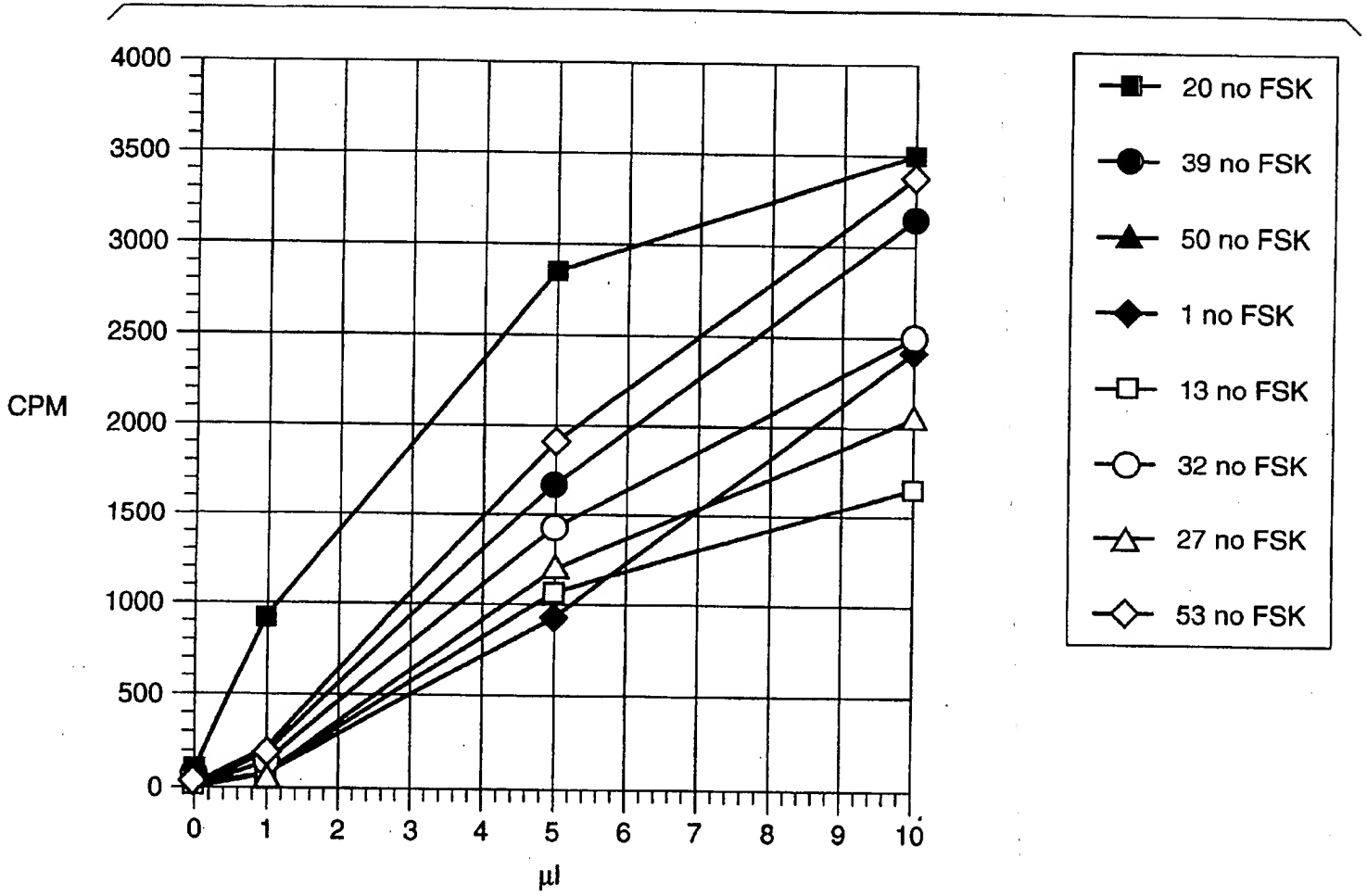

CPM
4000
3500
3000
2500
2000
1500
1000
500
0
0
1
2
3
4
5
6
7
8
9
10
µl
20 no FSK
39 no FSK
50 no FSK
1 no FSK
13 no FSK
32 no FSK
27 no FSK
53 no FSK

FIG. 48

Schwann Cell Assay/Baculovirus Clones

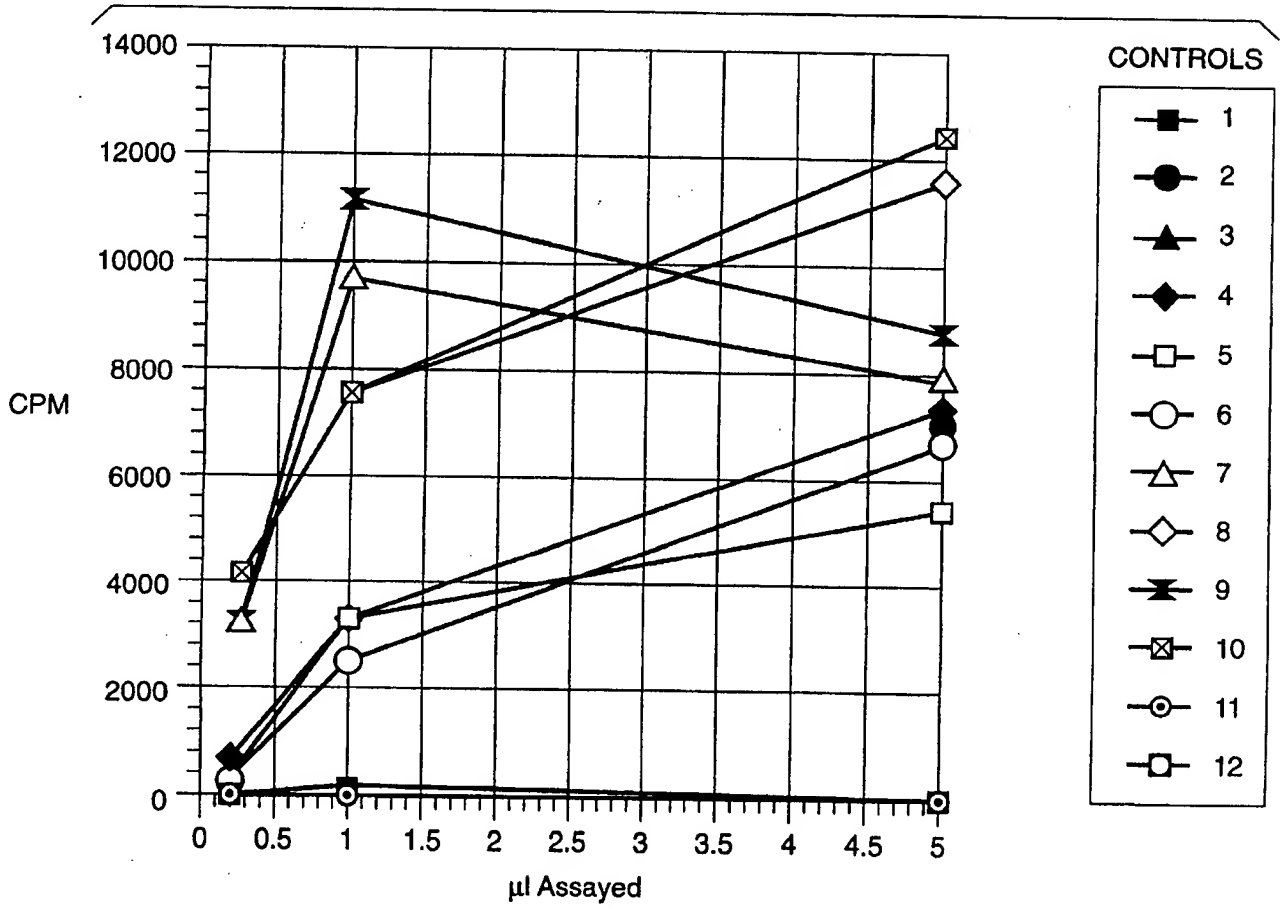


FIG. 49

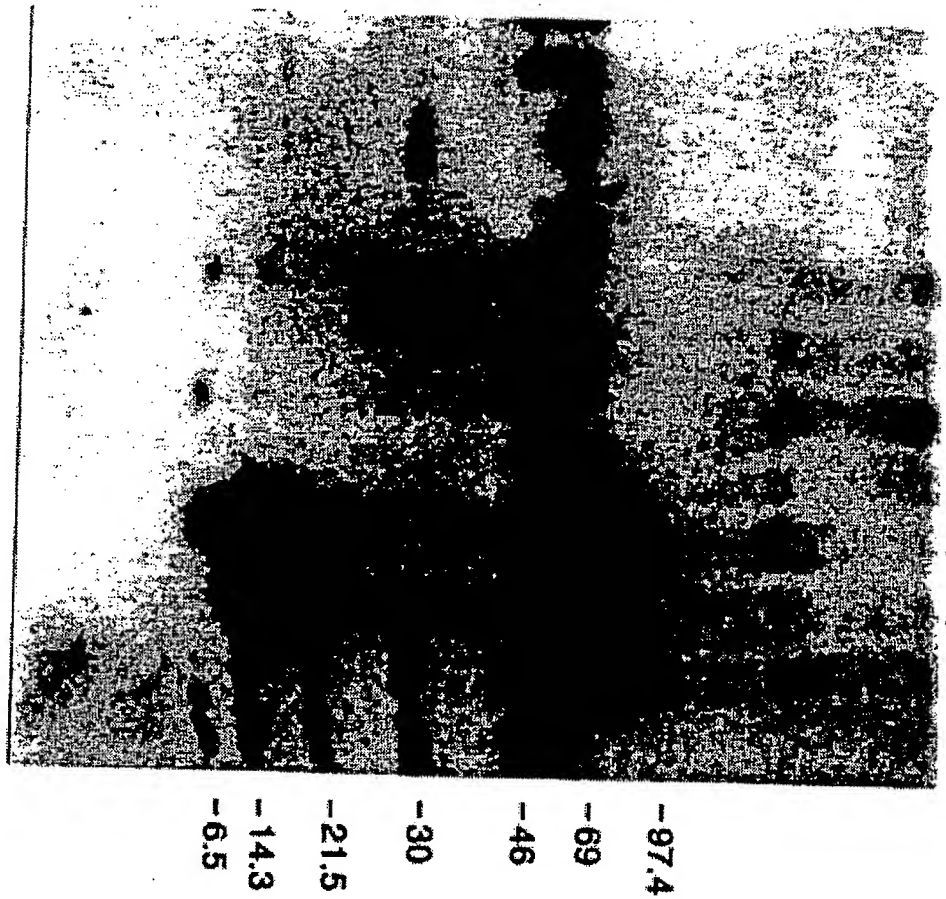

5—A2/3X B4
6—A2/2T ΔES MAXI 3
7—A2/2T ΔESI
8—BV 10 25 µl
9—BV 10 6µl
10—BV Control 25
11—BV Control 6
12—CHO HBS5
13—CHO Control
-6.5
-14.3
-21.5
-30
-46
-69
-97.4

FIG. 50A

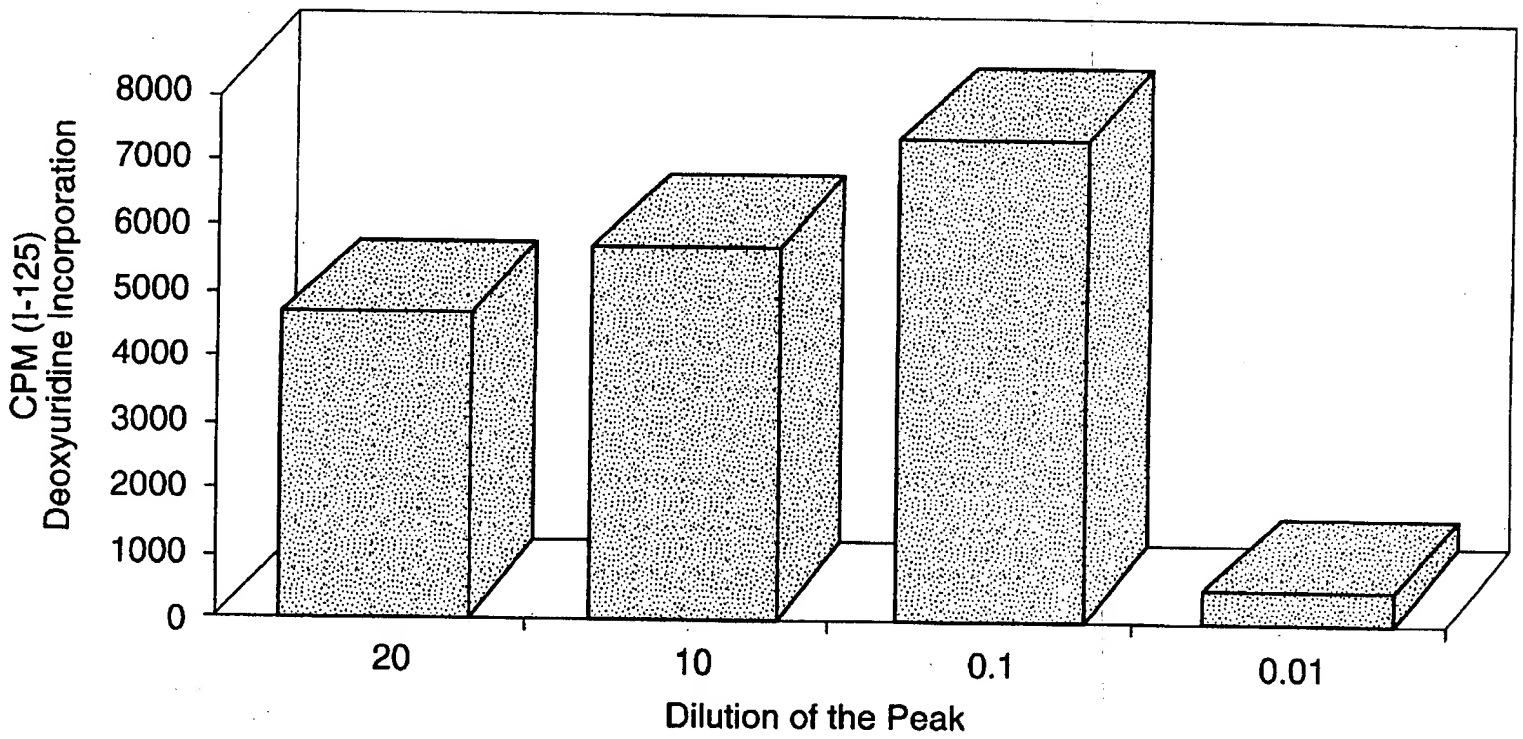

CPM (I-125) Deoxyuridine Incorporation
8000
7000
6000
5000
4000
3000
2000
1000
0
20
10
0.1
0.01
Dilution of the Peak

FIG. 50B

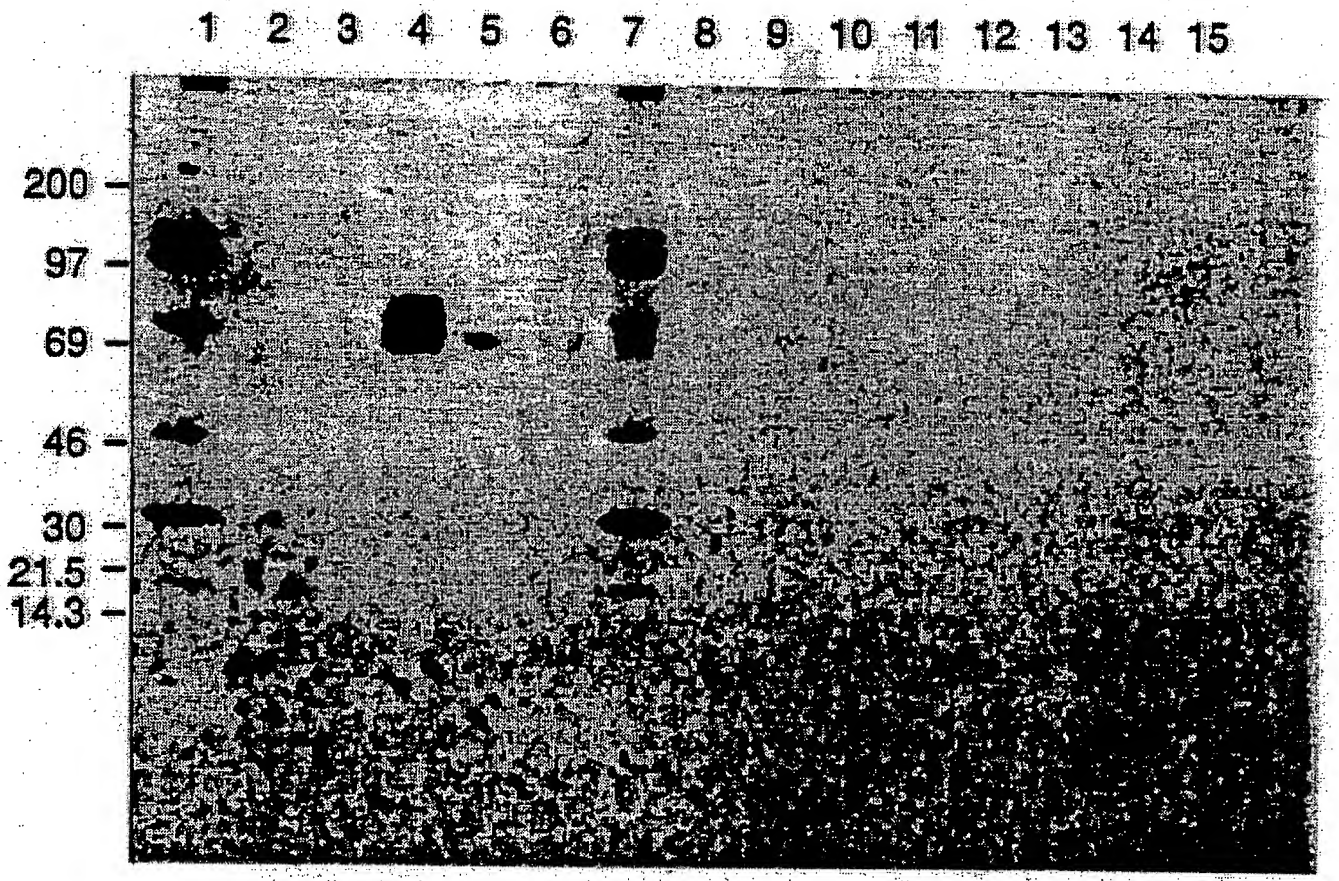


FIG. 51

rGGF Purification on Cation Exchange Column

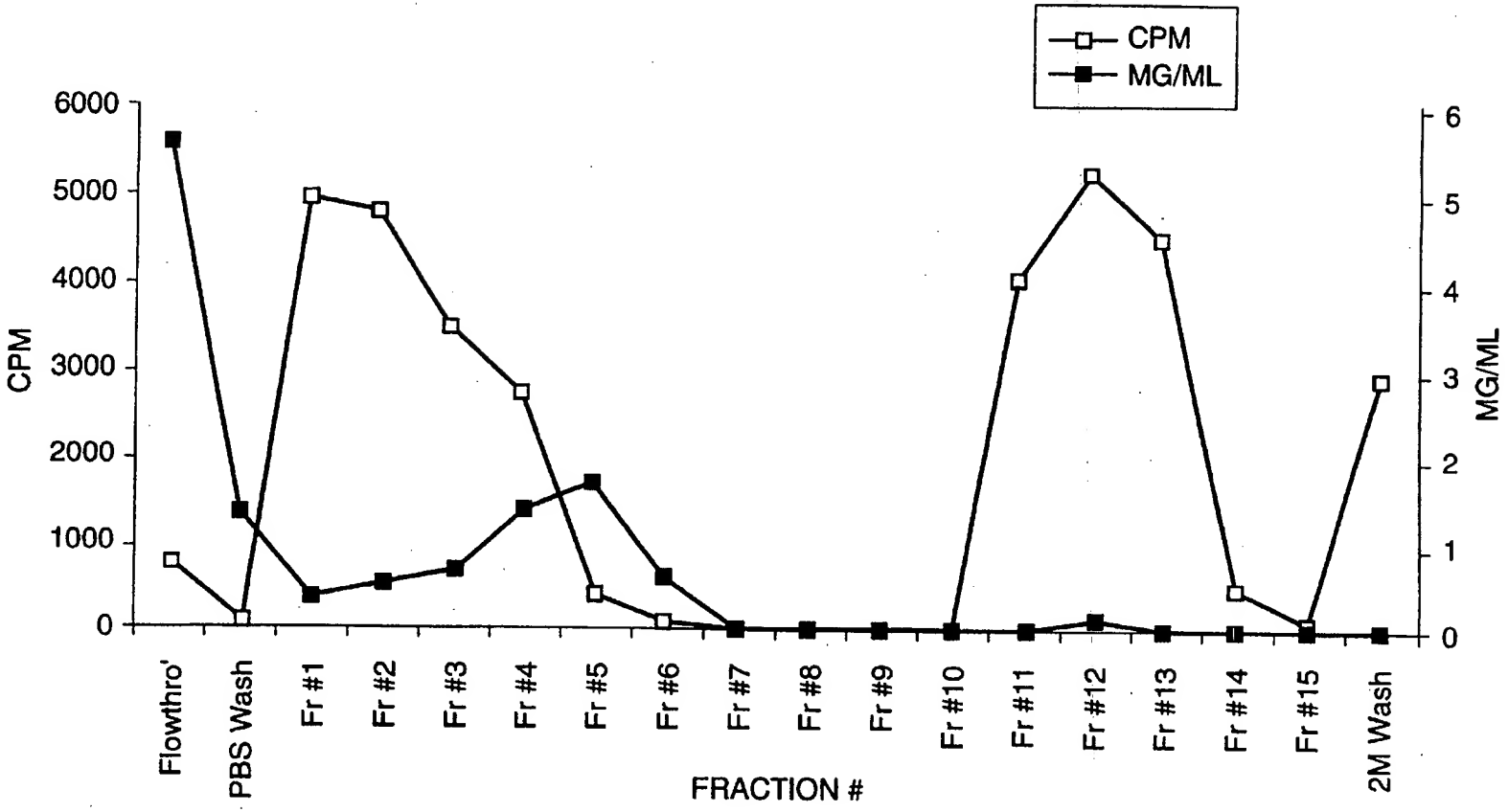


FIG. 51A

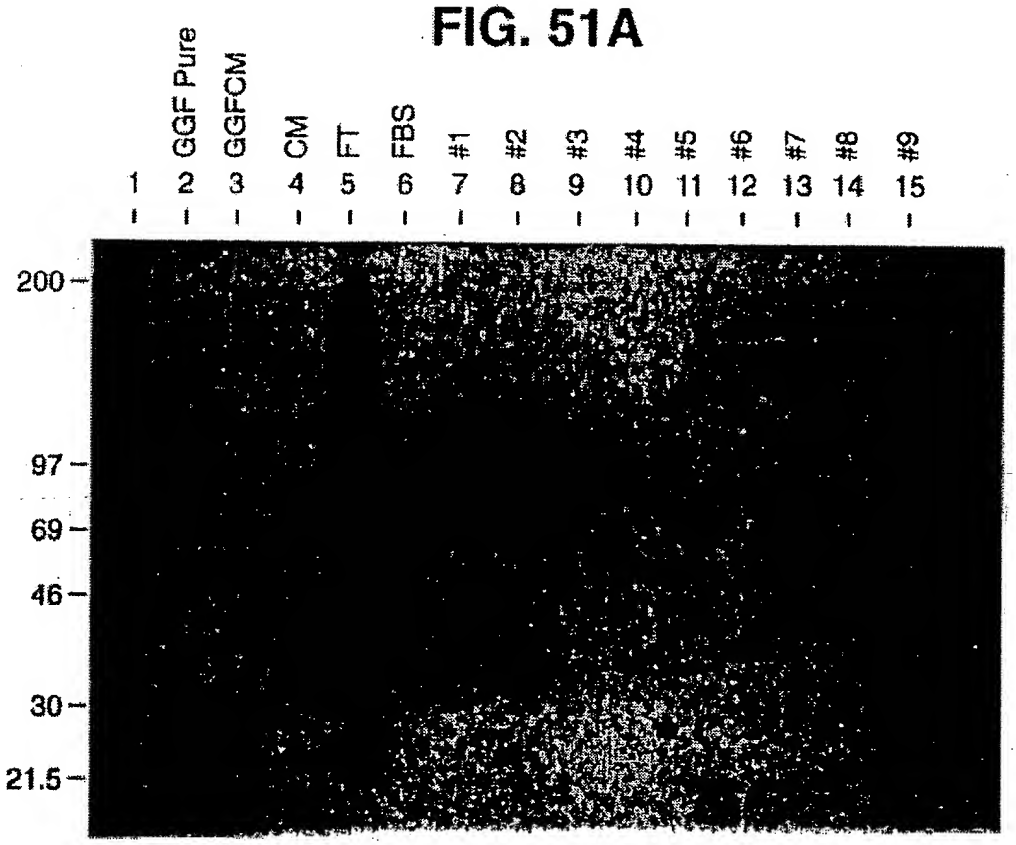


FIG. 51B

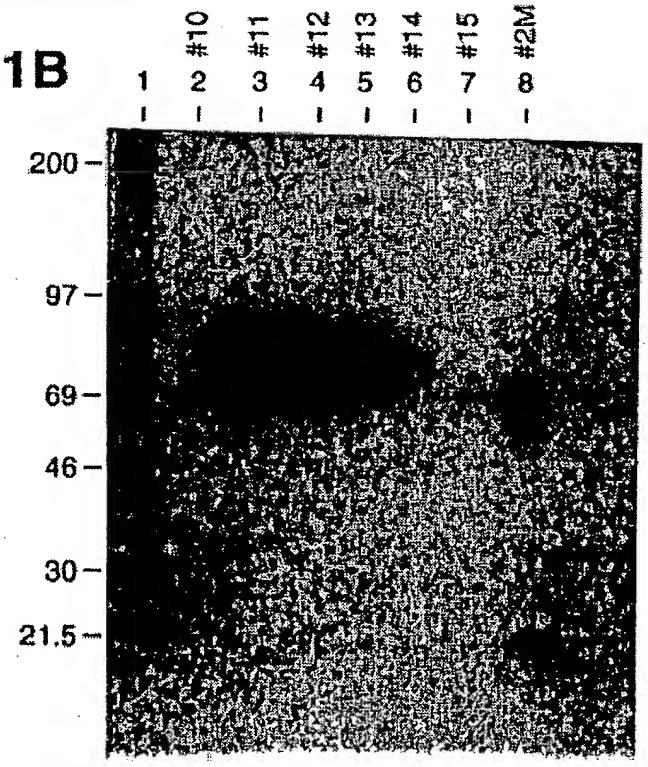
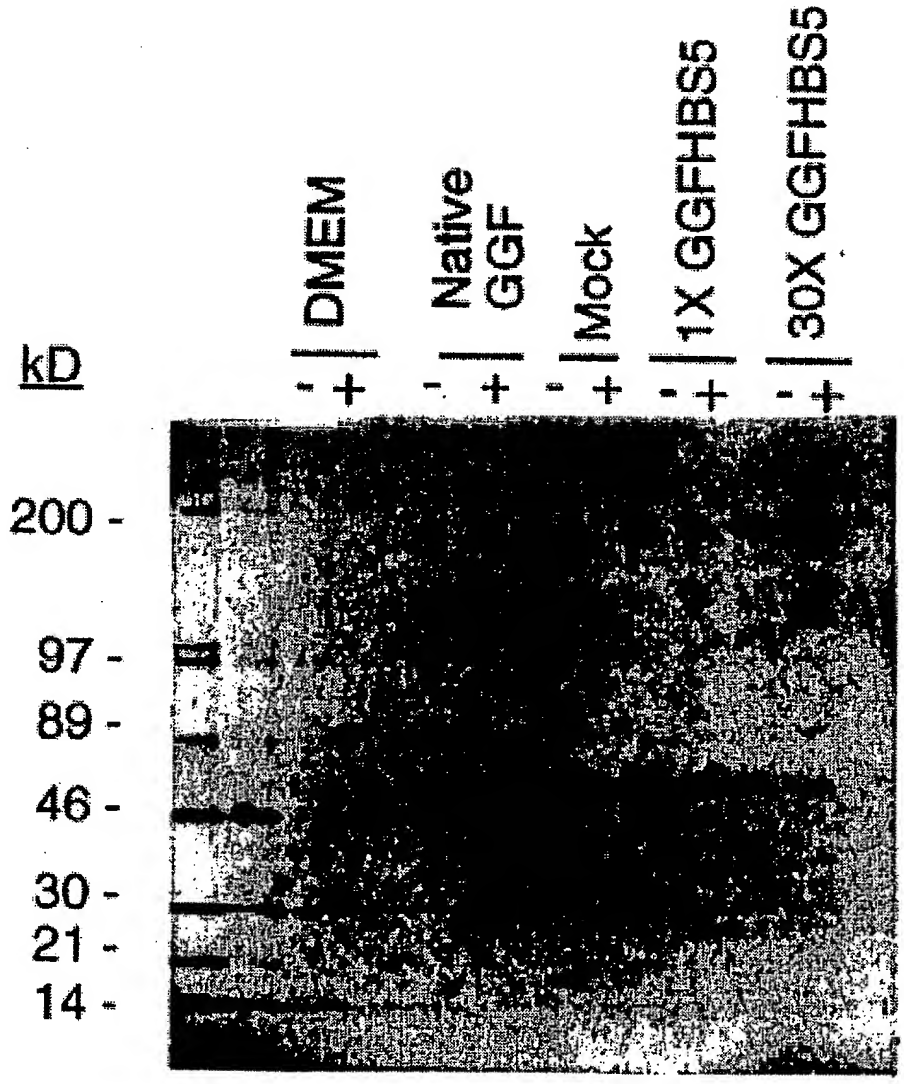


FIG. 52


kD
200 -
97 -
89 -
46 -
30 -
21 -
14 -
DMEM
Native GGF
Mock
1X GGFHBS5
30X GGFHBS5
- + - + - + - + - +

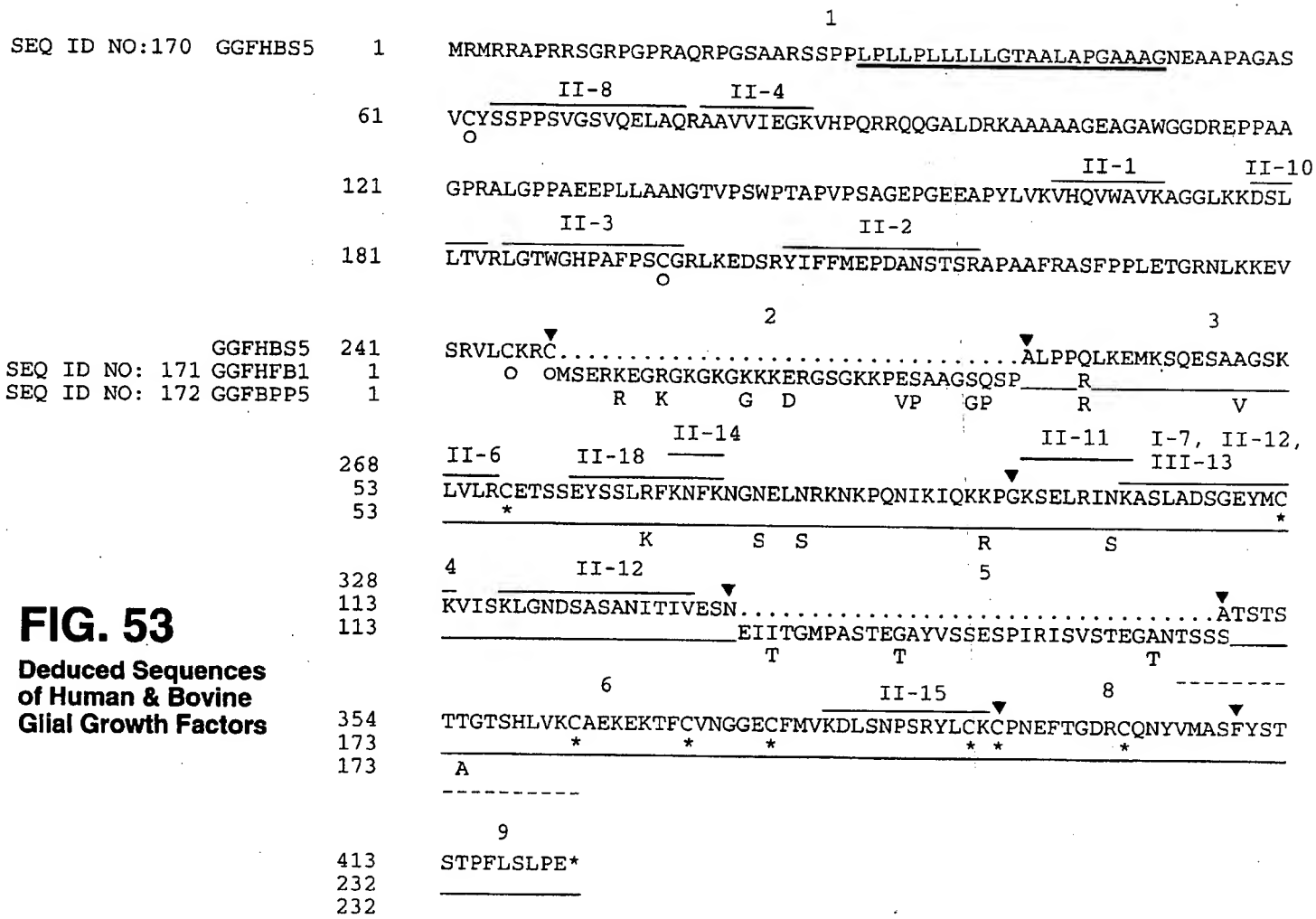
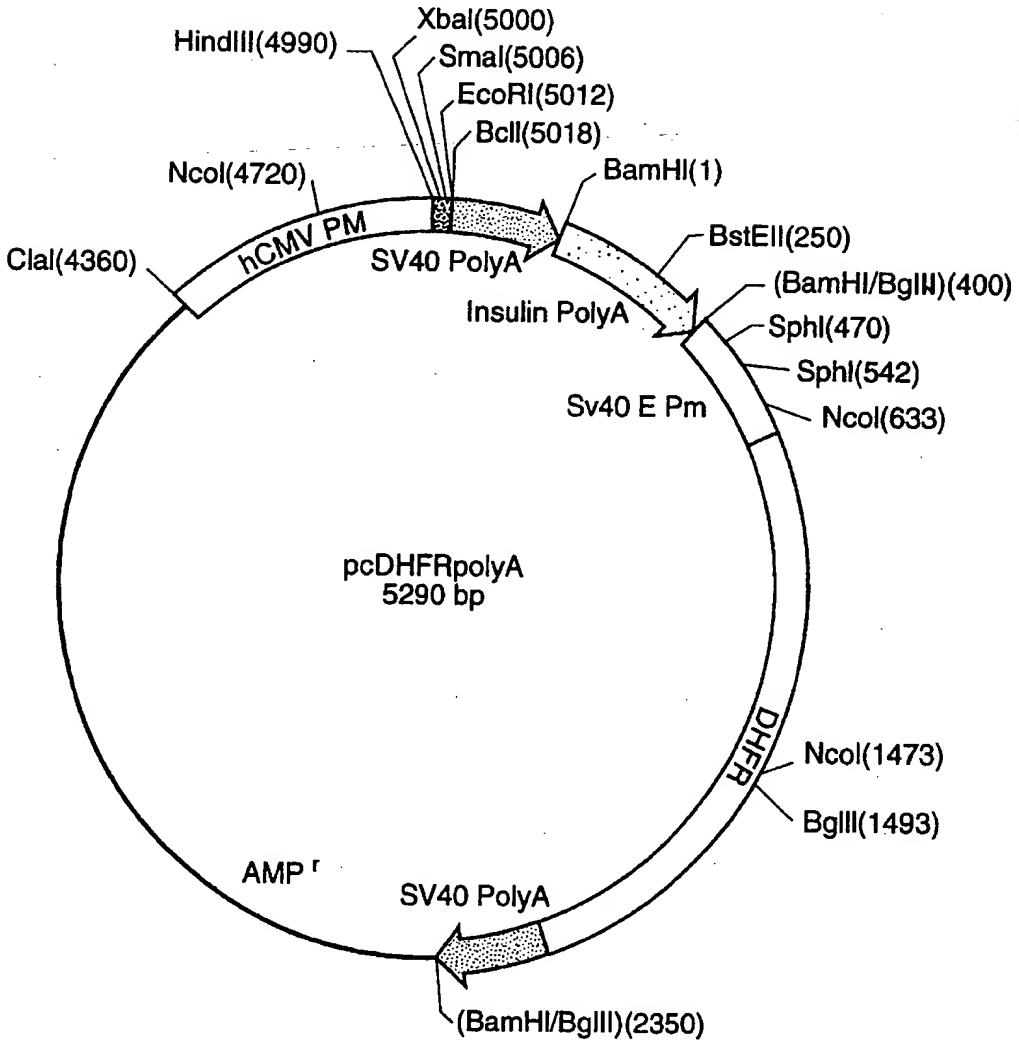


FIG. 53

Deduced Sequences of Human & Bovine Glial Growth Factors

FIG. 54


HindIII(4990)
XbaI(5000)
SmaI(5006)
EcoRI(5012)
BclI(5018)
NcoI(4720)
BamHI(1)
ClaI(4360)
hCMV PM
SV40 PolyA
BstEII(250)
(BamHI/BglII)(400)
Insulin PolyA
SphI(470)
SphI(542)
Sv40 E Pm
NcoI(633)
pcDHFRpolyA
5290 bp
DHFR
NcoI(1473)
BglII(1493)
AMP r
SV40 PolyA
(BamHI/BglII)(2350)